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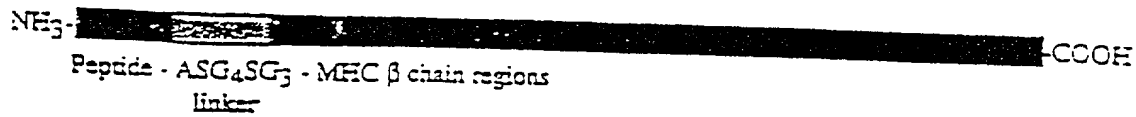
Figure 1A. Peptide-linker- β chain construct

Figure 1B. Schematic view of peptide-linked MHC binding groove

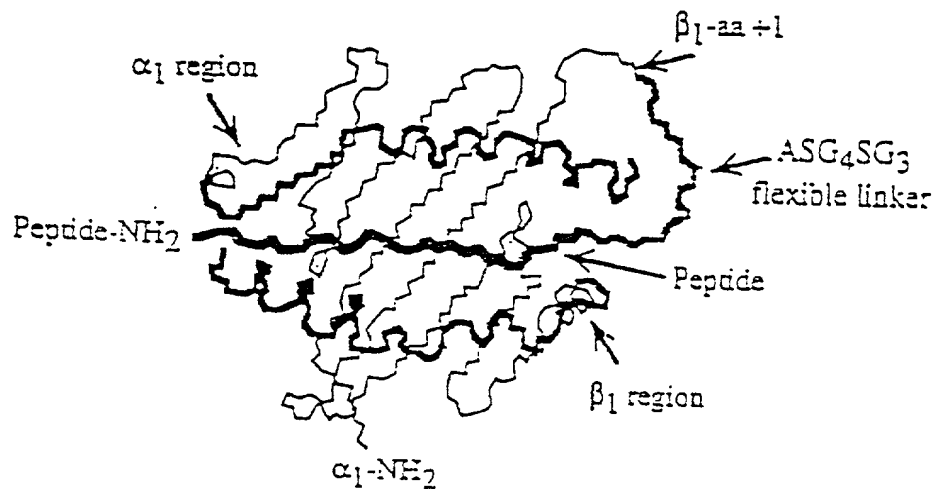
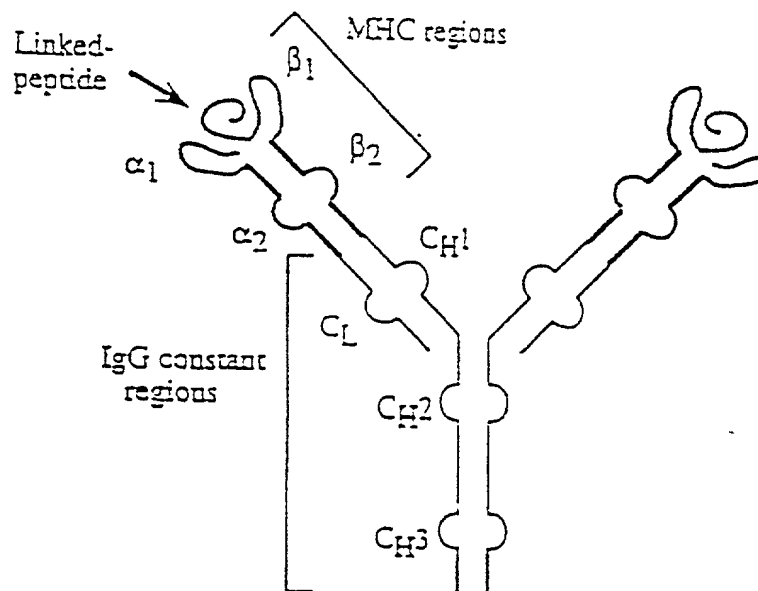
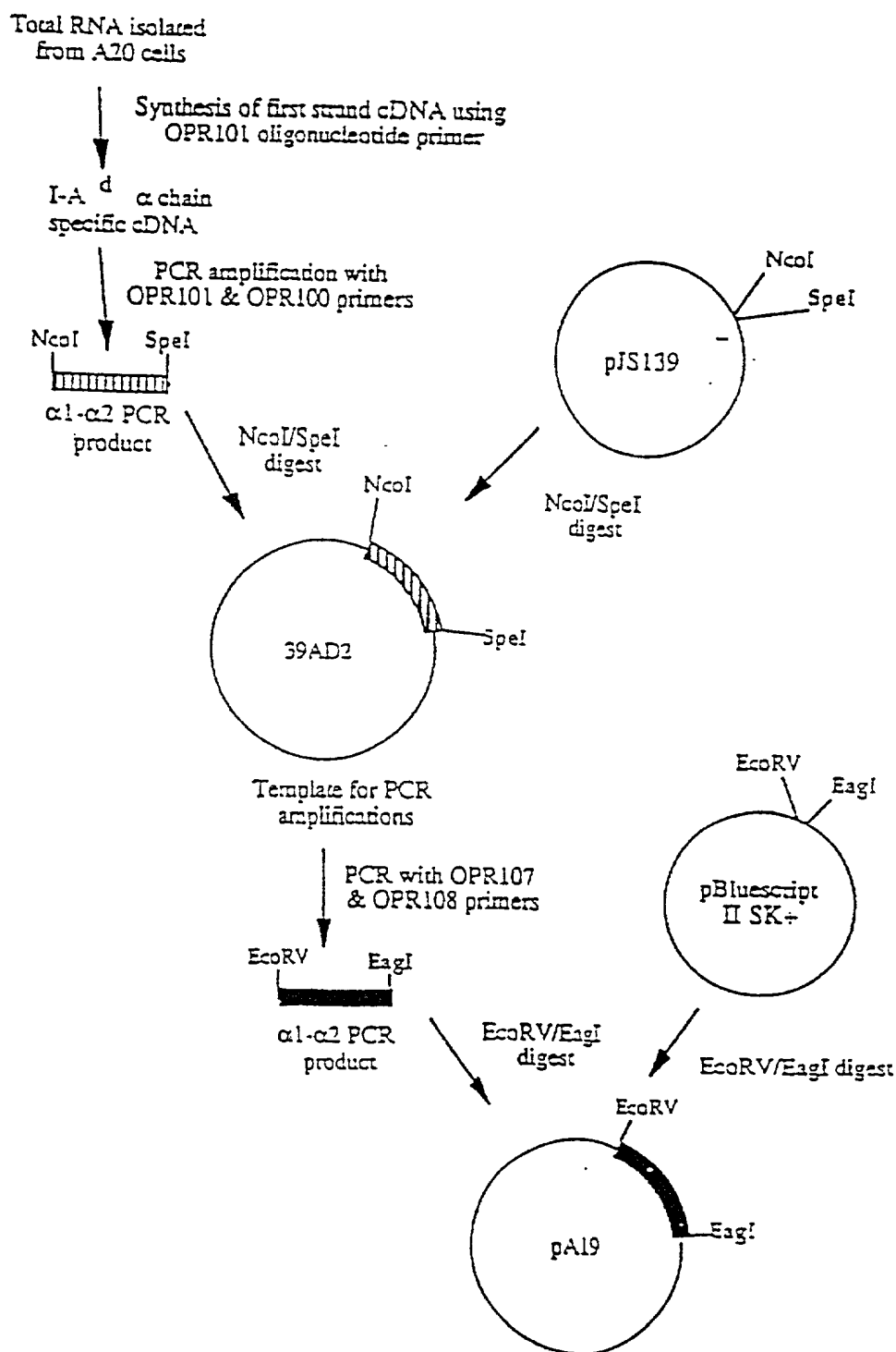


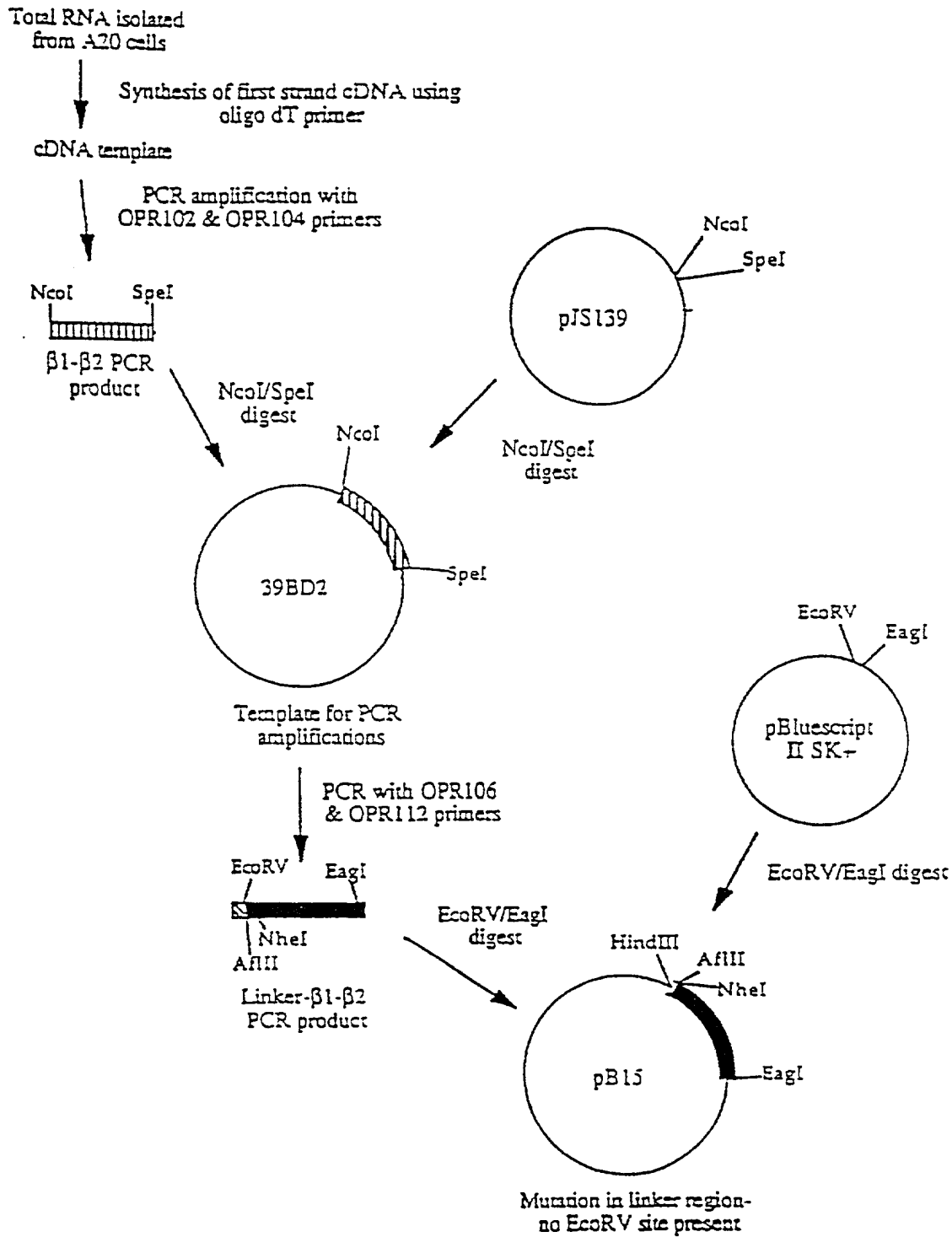
Figure 1C. Schematic view of soluble peptide-linked MHC-IgG C-region fusion protein



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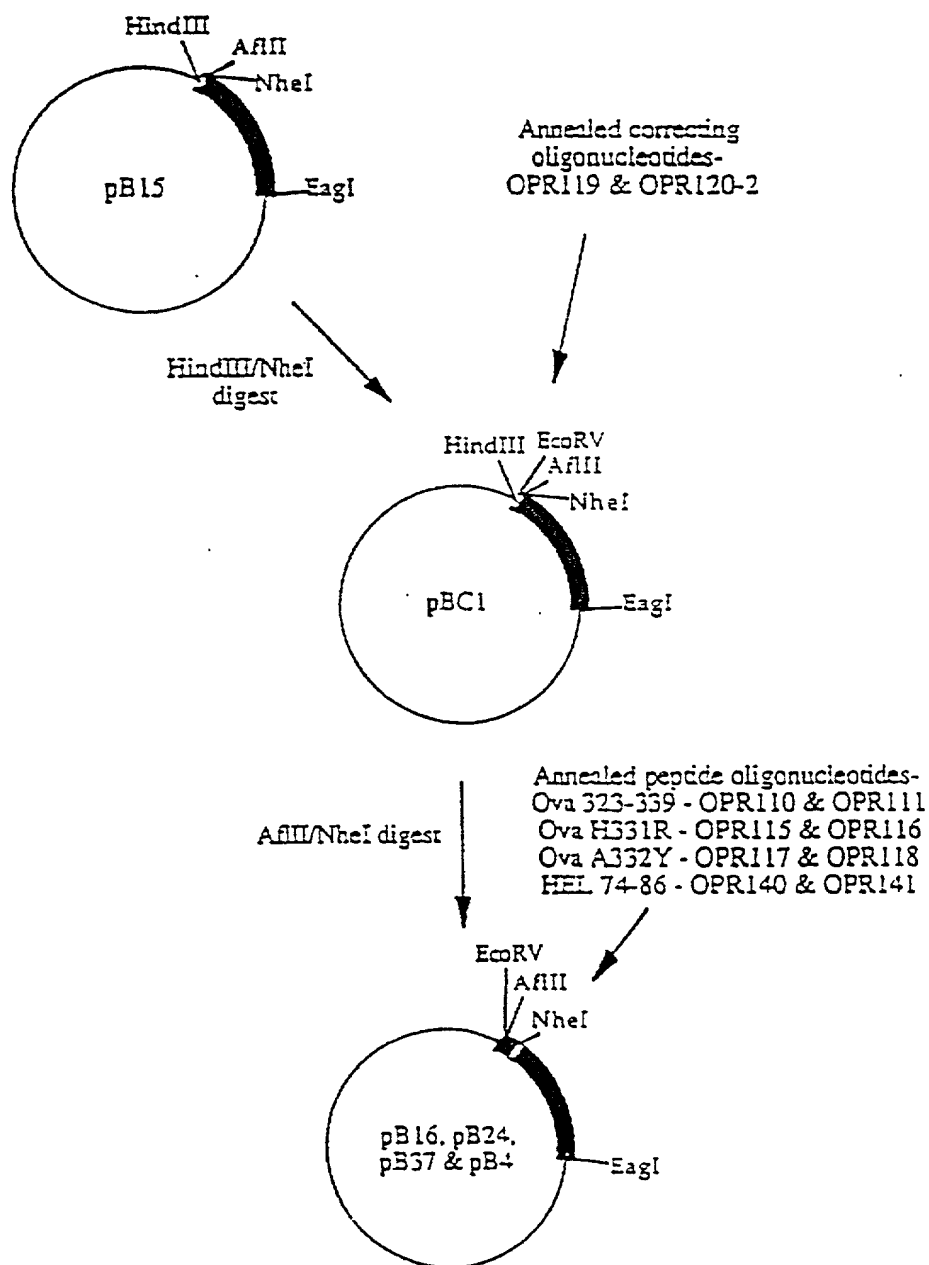
Figure 2: I-A^d α chain cloning scheme

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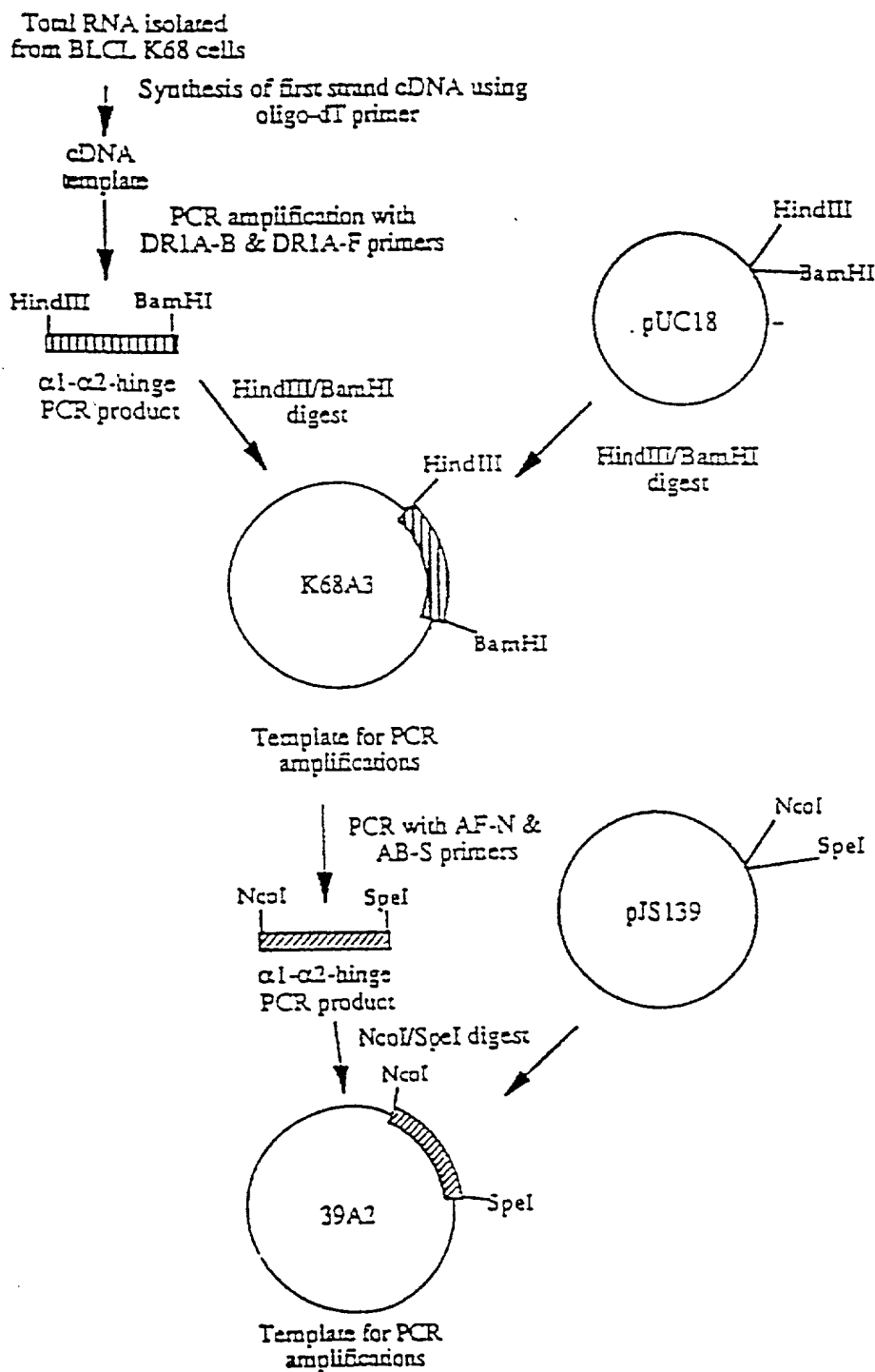
Figure 3: I-A^d β chain cloning scheme

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56

Figure 3: cont.

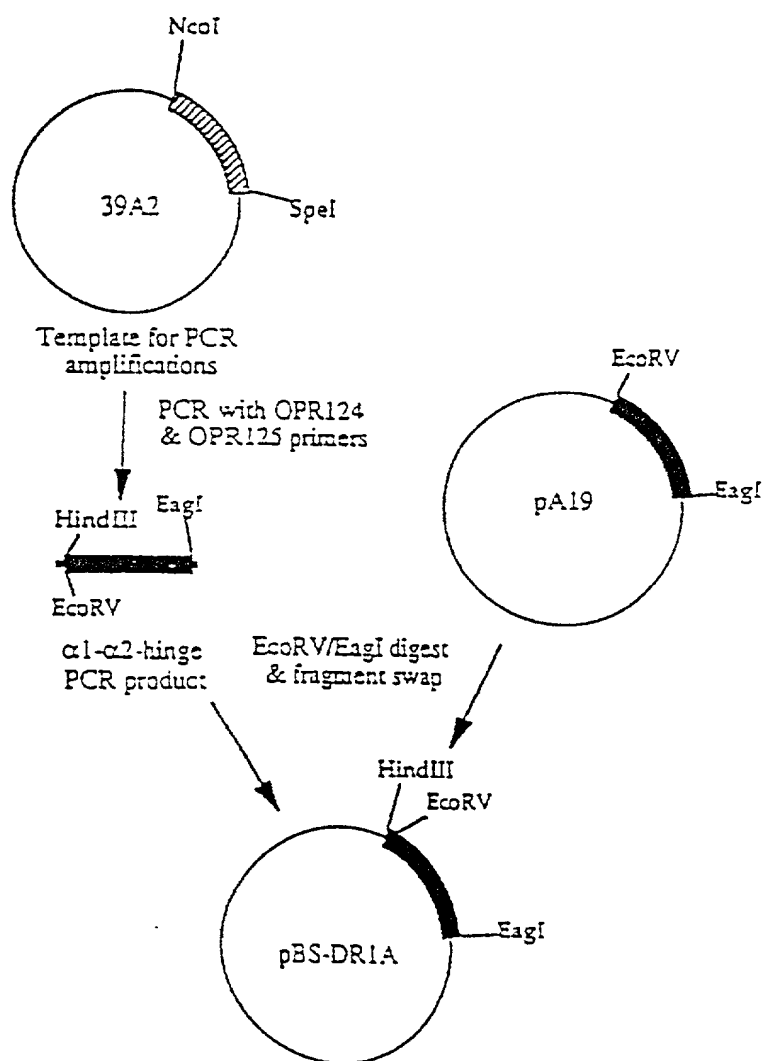


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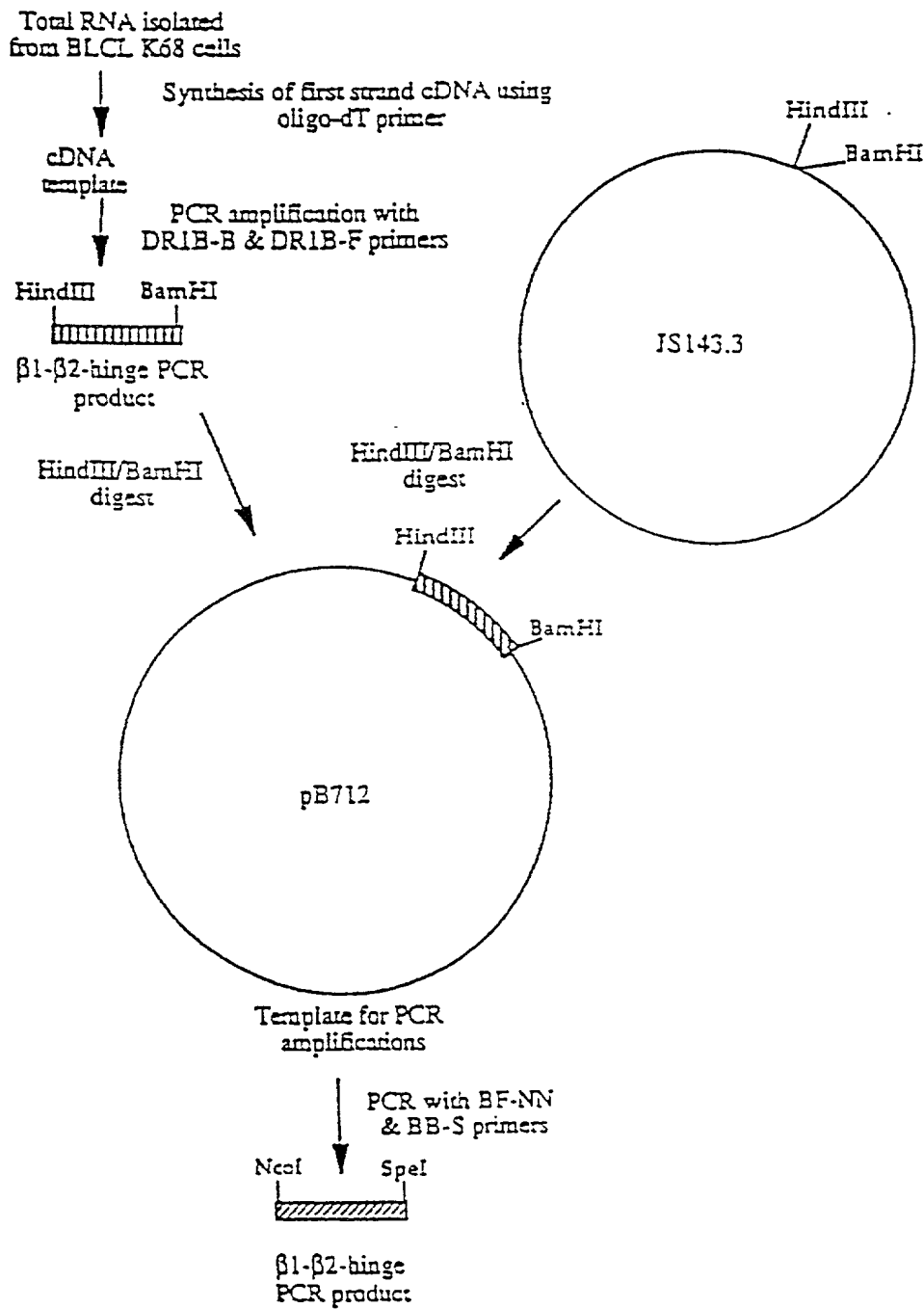
Figure 4: HLA-DR1 α chain cloning scheme

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Figure 4: cont.

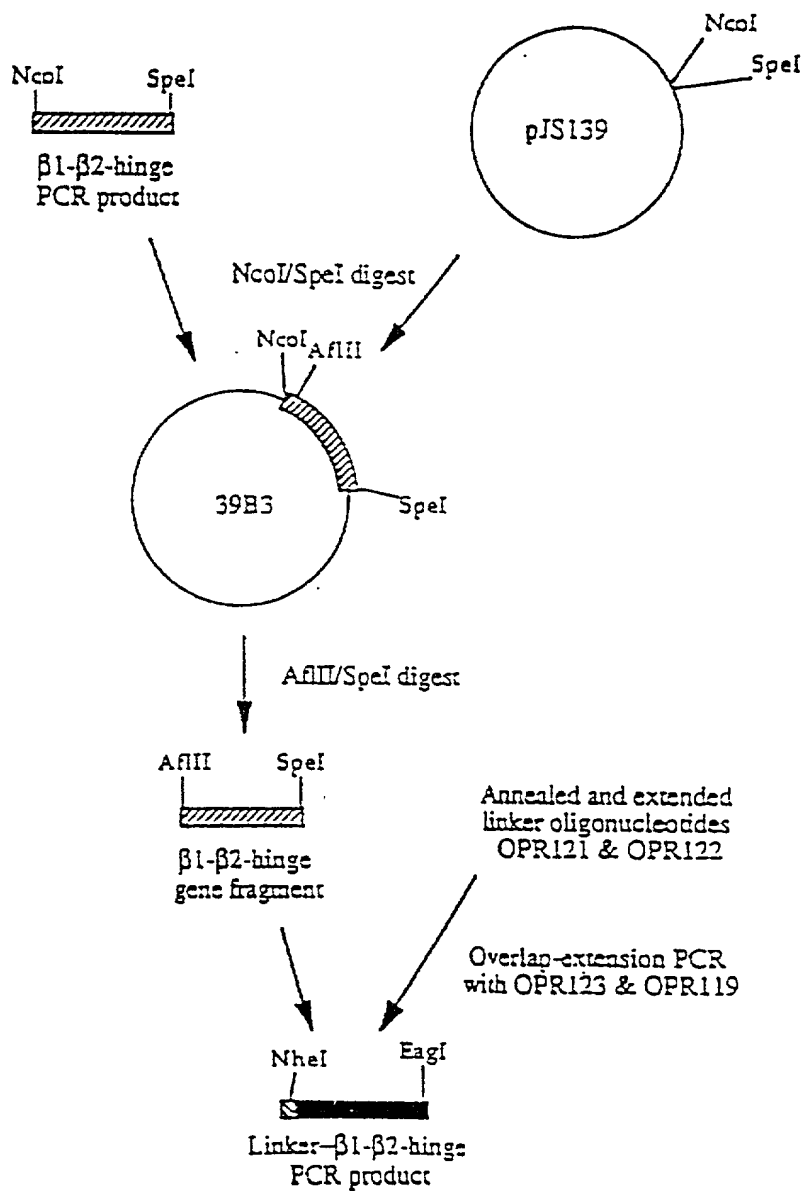


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Figure 5: HLA-DR1 β chain cloning scheme

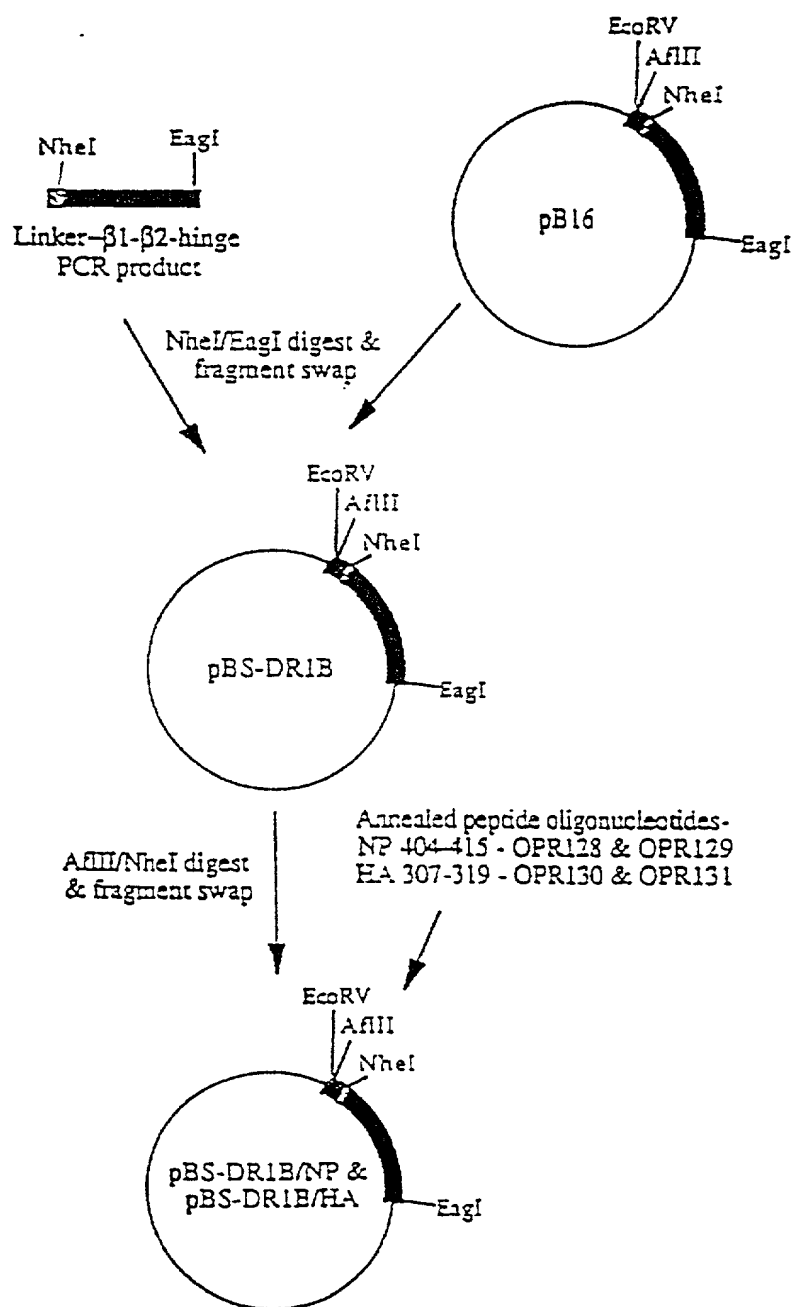
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Figure 5: cont.

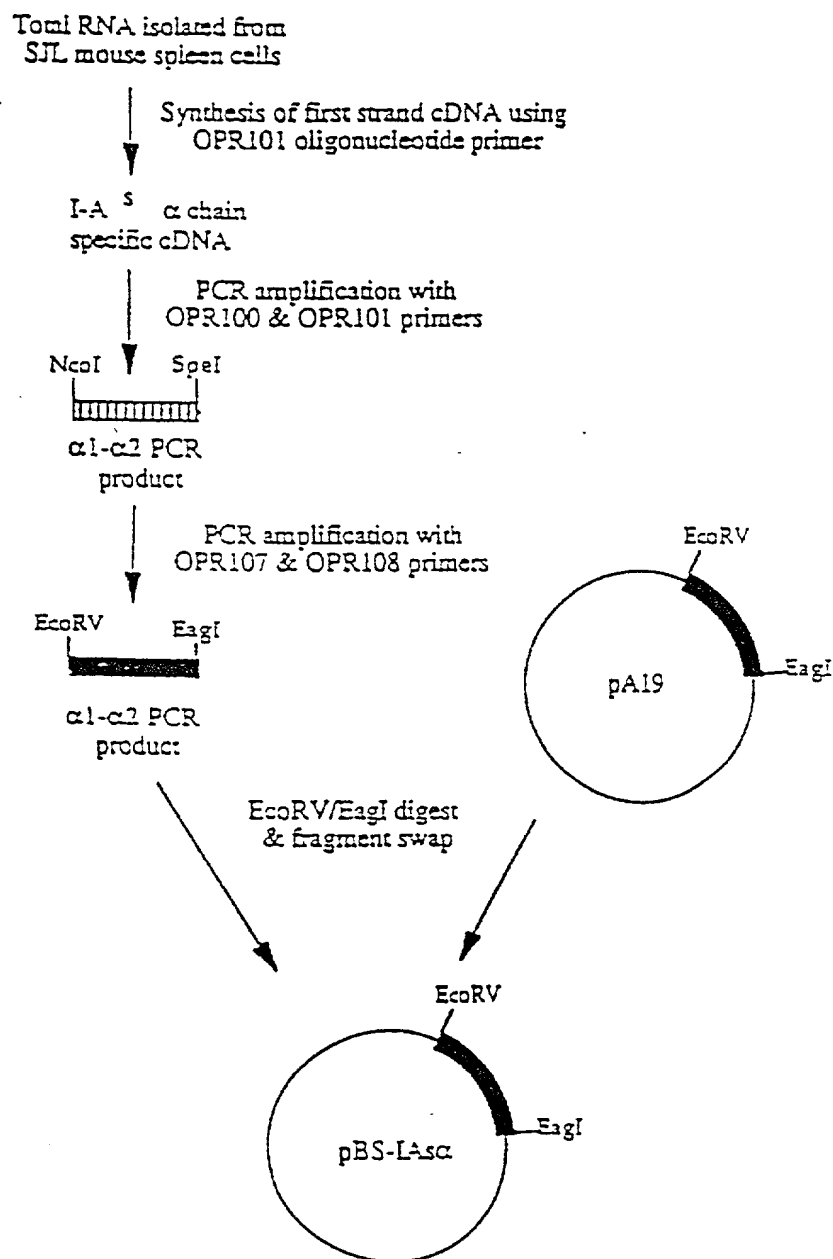


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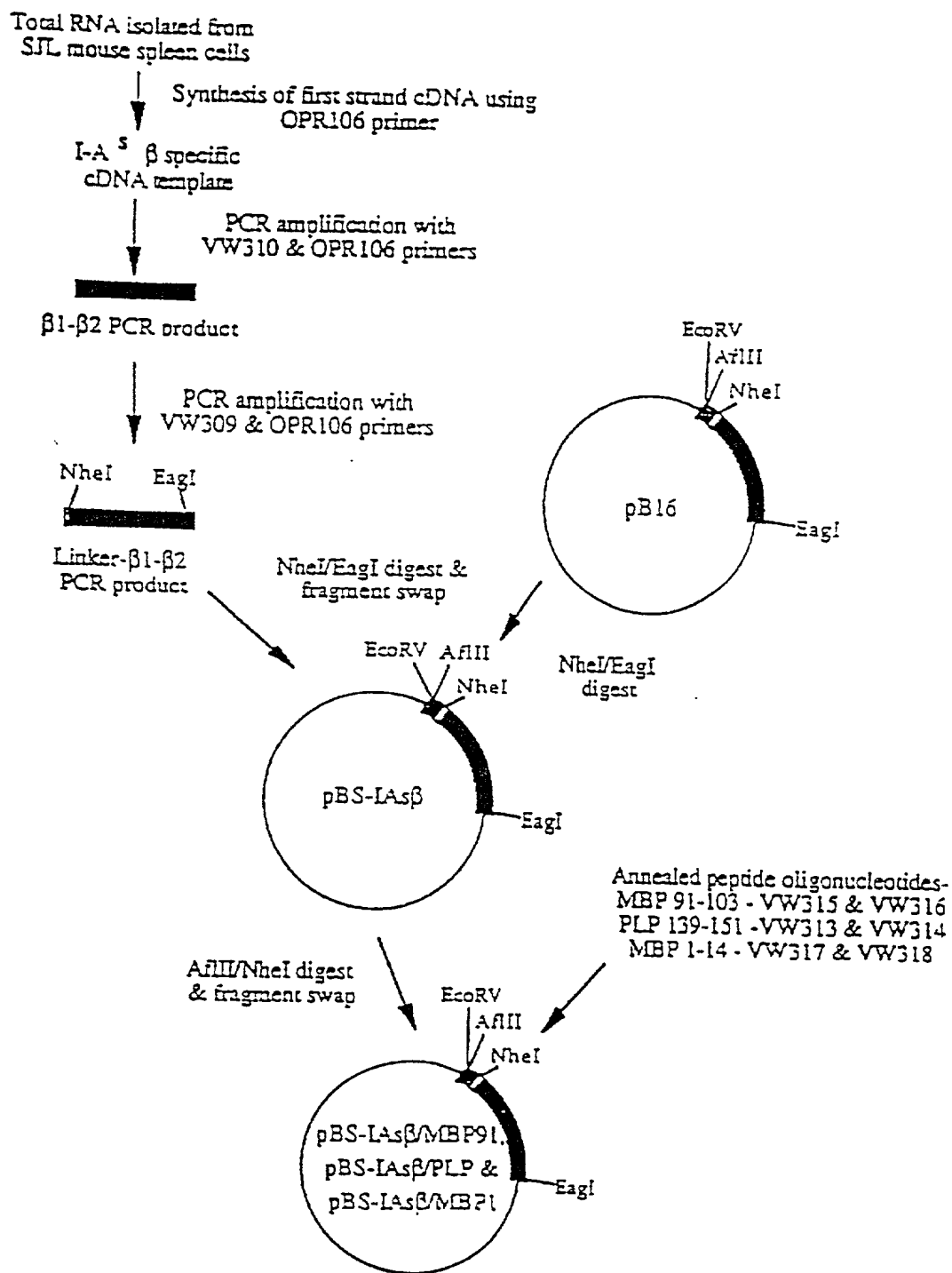
Figure 5: cont.



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Figure 6: I-A^S α chain cloning scheme

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Figure 7: I-A^S β chain cloning scheme

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Figure 8 - Oligonucleotides used in constructing MEC vectors

I-A⁴/I-A⁵ PCR primers and cloning oligonucleotides (restriction site are underlined).

OPR100

5'-GGG GGG GCC ATG GCC GAA GAC GAC ATT GAG GCC GAC-3'

OPR101

5'-GGG GCG ACT AGT CCA GTG TTT CAG AAC CGG CTC-3'

OPR107

5'-CCC CCC GAT ATC TCA GCT TCC AGC AGT GGA GAC GAC ATT GAG
GCC G-3'

OPR108

5'-CCC CCC CGG CCG CTA CTT ACG TTT CCA GTG TTT CAG AAC CGG
C-3'

OPR102

5'-GGG GGG GCC ATG GCC GGA AAC TCC GAA AGG CAT TTC G-3'

OPR104

5'-GGG GCG ACT AGT CCA CTC CAC AGT GAT GGG GC-3'

OPR106

5'-CCC CCC CGG CCG TAC CTG AGG ACC ACT CCA CAG TGA TGG-3'

OPR112

5'-CCC CCC GAT ATC ACA GGT GTC TTA AGT GCT AGC GGA GGG GGC
GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC-3'

OPR119

5'-AGC TTG ATA TCA CAG GTG TCT TAA GTG GAG-3'

OPR120-2

5'-CTA GCT CCA CTT AAG ACA CCT GTG ATA TCA-3'

VW310

5'-TCC GGA GGC GGC GGA GAC TCC GAA AGG CAT TTC G-3'

VW309

5'-CCA TCG CTA GCG GCG GTG GTG GTT CCG GTG GCG GCG GAG-3'

OPR136

5'-CCC CCC AGG CTT CCC GGG CCA CCA TGC CGT GCA GCA GAG CTC
TG-3'

OPR139

5'-CCC CCC GAG CTC GAA TTC TCA TAA AGG CCC TGG GTG TCT G-3'

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Figure 3 - cont.

OPR132

5'-CCC CCC AAG CTT CCC GGG CCA CCA TGG CTC TGC AGA TCC CCA
GC-3'

OPR133

5'-CCC CCC ACT TAA GGT CCT TGG GCT GCT CAG CAC C-3'

OPR134

5'-CCC CCC CCA TCA CTG TGG AGT GGA GGG-3'

OPR135

5'-CCC CCC GAG CTC GAA TTC TCA CTG CAG GAG CCC TGC TGG-3'

HLA-DR1 PCR primers and cloning oligonucleotides.

DR1A-F

5'-GGG GGG AAG CTT ATG ATC AAA GAA GAA CAT GTG ATC ATC-3'

DR1A-B

5'-GCG GCG GGA TCC GTT CTC TGT AGT CTC TGG GAG AGG-3'

DR1B-F

5'-GGG GGG AAG CTT ATG GGG GAC ACC CGA CCA CGT TTC TTG TGG
CAG C-3'

AF-N

5'-GGG GGG GCC ATG GCC ATC AAA GAA GAA CAT GTG ATC ATC-3'

AB-S

5'-GCG GCG ACT AGT GTT CTC TGT AGT CTC TGG GAG AGG-3'

OPR124

5'-GGG GGG AAG CTT GAT ATC TCA GCT TCC AGC AGT AGT ATC AAA
GAA GAA CAT GTG ATC-3'

OPR125

5'-GGG GGG CGG CCG CTA CTT ACC TTT CTC TGG GAG AGG GCT TGG
AGC-3'

DR1B-B

5'-GCG GCG GGA TCC CTT GCT CTG TGC AGA TTC AGA CC-3'

BF-NN

5'-GGG GGG GCC ATG GCC GGA TCC GCT AGC GGG GAC ACC CGA CCA
CGT TTC TTG-3'

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Figure 3 - cont.

BB-5

5'-GCG GCG ACT AGT CTT GCT CTG TGC AGA TTC AGA CCG-3'

OPR121

5'-GTT GTC TTA AGT GGA GCT AGC GGA GGG GGC GGG TCC GGA GGT
GGT GGG GAC ACC CG-3'

OPR122

5'-GAA ATG ACA TTC AAA CTT CAG CTG CCA CAA GAA ACG TGG TCG
GGT GTC CCC ACC ACC-3'

OPR123

5'-GGG GGG CGG CCG TAC CTG AGG ACT TGC TCT GTG CAG ATT CAG-
3'

Peptide oligonucleotides.

Ova 323-339

OPR110

5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CAC GCT GAA ATC
AAC GAA GCT GGT CGT G-3'

OPR111

5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA GCC TGA GCA GCG TGA
ACA GCC TGA GAG ATA C-3'

Ova H331R

OPR115

5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CGG GCT GAA ATC
AAC GAA GCT GGT CGT G-3'

OPR116

5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA GCC CGA GCA GCG TGA
ACA GCC TGA GAG ATA C-3'

Ova A332Y

OPR117

5'-TTA AGT ATC TCT CAG GCT GTT CAC GCT GCT CAC TAC GAA ATC
AAC GAA GCT GGT CGT G-3'

OPR118

5'-CTA GCA CGA CCA GCT TCG TTG ATT TCA TAG TGA GCA GCG TGA
ACA GCC TGA GAG ATA C-3'

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Figure 8 - con.

HEL 74-86

CPRI40

5'-TTA AGT AAC CTG TGC AAC ATC CCC TGC AGC GCC CTG CTG AGC
TCC G-3'

OPR141

5'-CTA GCG GAG CTC AGC AGG GCG CTG CAGGGG ATG TTG CAC AGG
TTA C-3'

NP 404-115

CPR:28

5' -TTA AGT CAG ATC AGC GTG CAG CCC GCC TTC AGC GTG CAG G-3'

OPR:29

5'-CTA GCC TGC ACG CTG AAG GCG GGC TGA ACG CTG ATC TGA C-3'

HA 307-319

CPR 130

5'-TGA AGT CCC AAG TAC GTG AAG CAG AAC ACC CTG AAG CTG GCC
ACC G-3'

CPR131

5'-CTA GCG GTG GCC AGC TTC AGG GTG TTC TGC TTC ACG TAC TTG
GGA C-3'

MBP 91-103

VW31E

5'-TTA AGT CAC TAT GGC TCC CTG CCG CAG AAG TCC CAG CAC GGG
CGC G-3'

VW316

5' -CTA GCG CGC CCG TGC TGG GAC TTC TGC GGC AGG GAG CCA TAG
TGA C-3'

PLP 139-151

VW313

S'-TTT CAT CAC TCC CTG GGC AAG TGG CTG GGC CAC CCG GAC AAG
TTC G-3'

VW3:4

5'-CTA GCG AAC TTG TTC GGG TGG CCC AGC CAC TTG CCC AGG GAG
TGA C-3'

Figure 1 consists of 12 histograms arranged in a single column. Each histogram represents the distribution of the number of non-zero elements in the vector x for a specific value of n . The values of n are 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, and 120, labeled on the right side of each plot. The x-axis for all plots is labeled 'Number of non-zero elements' and ranges from 0 to 120. The y-axis is labeled 'Frequency' and ranges from 0 to 120. As n increases, the distribution of non-zero elements shifts to the right, with the peak frequency increasing and the spread of the distribution widening.

Figure 8 - cont.

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MBP 1-14

VW317

5'-TGA AGT ATG GCA TCC CAG AAG CGC CCG TCC CAG CGC TCC AAG
TAC CTG G-3'

VW316

5'-CTA GCC AGG TAC TTG GAG CGC TGG GAC GGG CGC TTC TGG GAT
GCC ATA C-3'

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ECGRV										XbaI									
10										580									
GATATATGAGCT										GATATGAGCTGCT									
AGC AGT GAA GAC AAT GAG GCG GAC CAC										GCT GTC GTC AAA CAC TGG AAA GCT AAGTAGAGGGGGG									
CTATAGAGCTGCA										AGG TGG TCA CTT CTT TAA CTT CCG CTT GTC									
S S S E D D I E A D R										// P V L K H W K R									
-1										aa192									
IgG κ chain										I-α ^c α chain									
Signal peptide										IgG κ chain									
Cleavage site										aa558									

Soluble I-A^d β chain construct

EcoRV AclII NheI

10 20 30 40 50 60 70

GATATCAGCGT GTC TTA AGT CGA GCT AGG CGA GGG GGC GGA AGC GGC CGA GGG CGA AAC TTC TGA AGG CAT //

CCTACGTCTGCA CAG AAT TCA GGT CGA TGG GGT GGG GGC GGT TTC GGC GGT GGT TTC AGG GTT TCC GTA //

V L S ↑ G A S G G G G S G G G G N S E R H //

IgG H chain Signal peptide Linker region I-AB β chain

Intron cleavage site

XbaI

610 620 630

ATC ACT CTC GAG TGC TTC TCA GGT ACNCCCCCG

TAG TGA CAC CTC ACC AGG ACT CGA TCCCCCCCC

I T V E W S S

aa189|

I-AB β chain IgG H chain

Intron

Soluble I-AS \propto chain construct

ECDRV
 10 20 30 40 50 60 70 80
 GATATGTCAGGT TGG AGC AGT GAA GAC GAC ATT GAG GCG GAC GAC // GCG GTT GTG AAA CAC TGG AAA COT AAGTAGCGGGGGG
 CTTATAGACTGTA AGG TGG TCA GTT GTG GTC TAA GTT GCG GTG GTG // GCG CAA GAC TTT GTG AGC TTT GCA TGTATCGCGGGG
 S S S E D D I E A D K // P V L K H W K R
 -1
 IgG κ chain Signal peptide I-A⁵ α chain IgG κ chain
 100000 100000
 Cleavage site

Figure 9 - cont.

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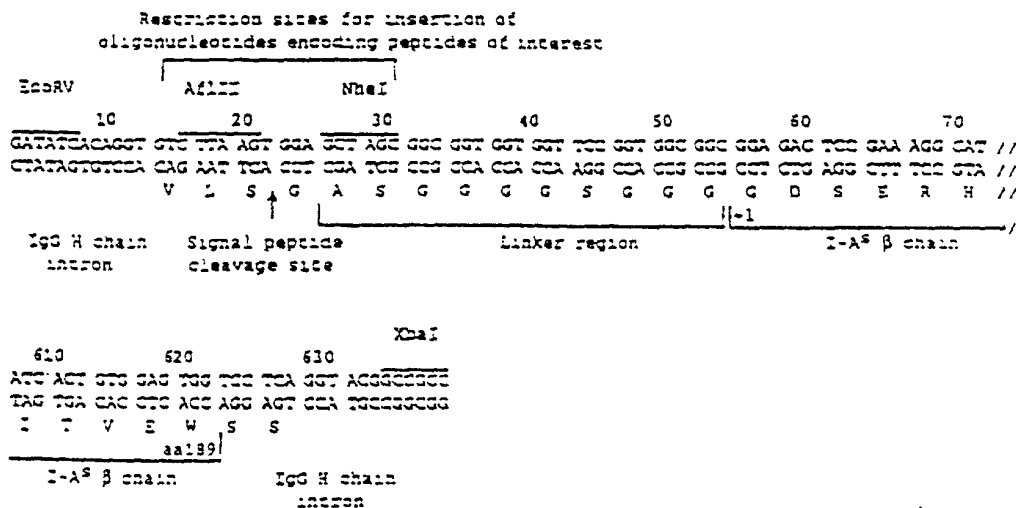
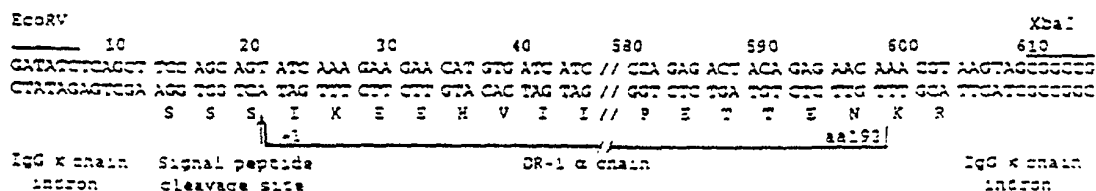
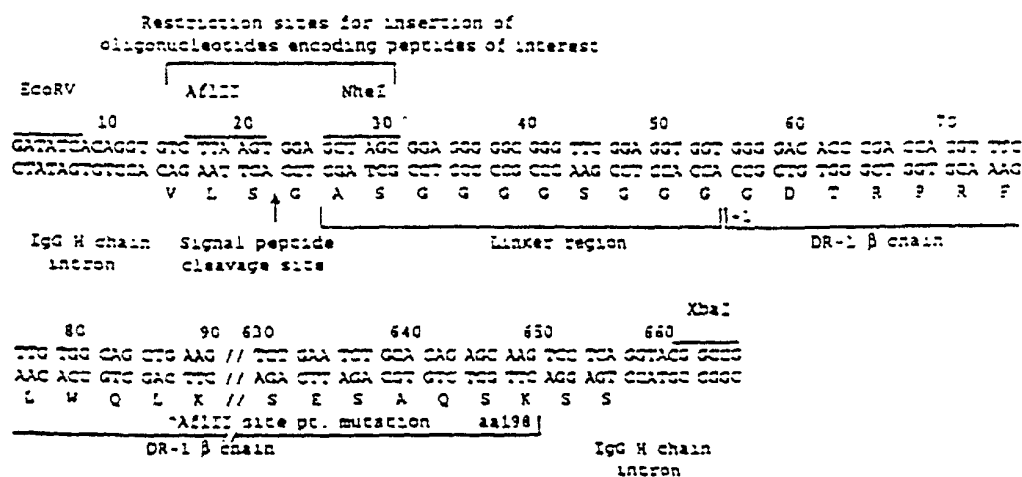
Figure 9D. Soluble I-A^s β chain constructFigure 9E. Soluble HLA-DR1 α chain constructFigure 9F. Soluble HLA-DR1 β chain construct

Figure 10A

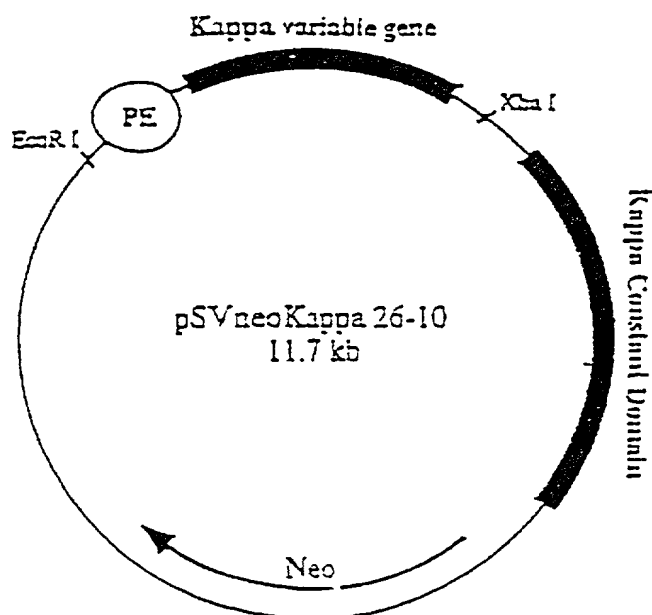
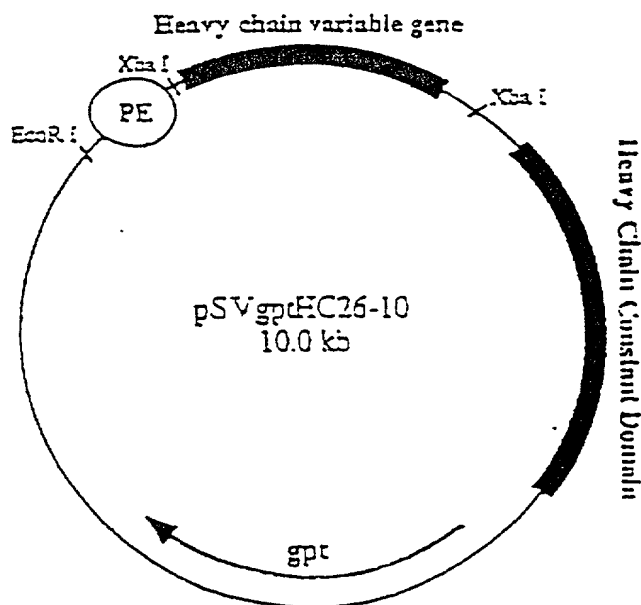
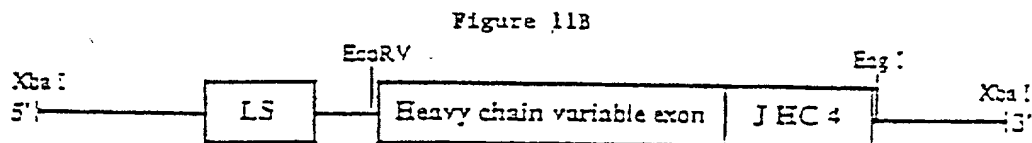
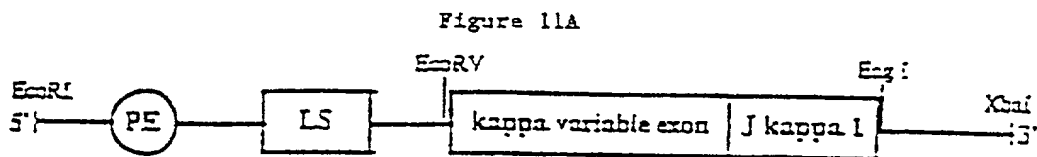


Figure 10B



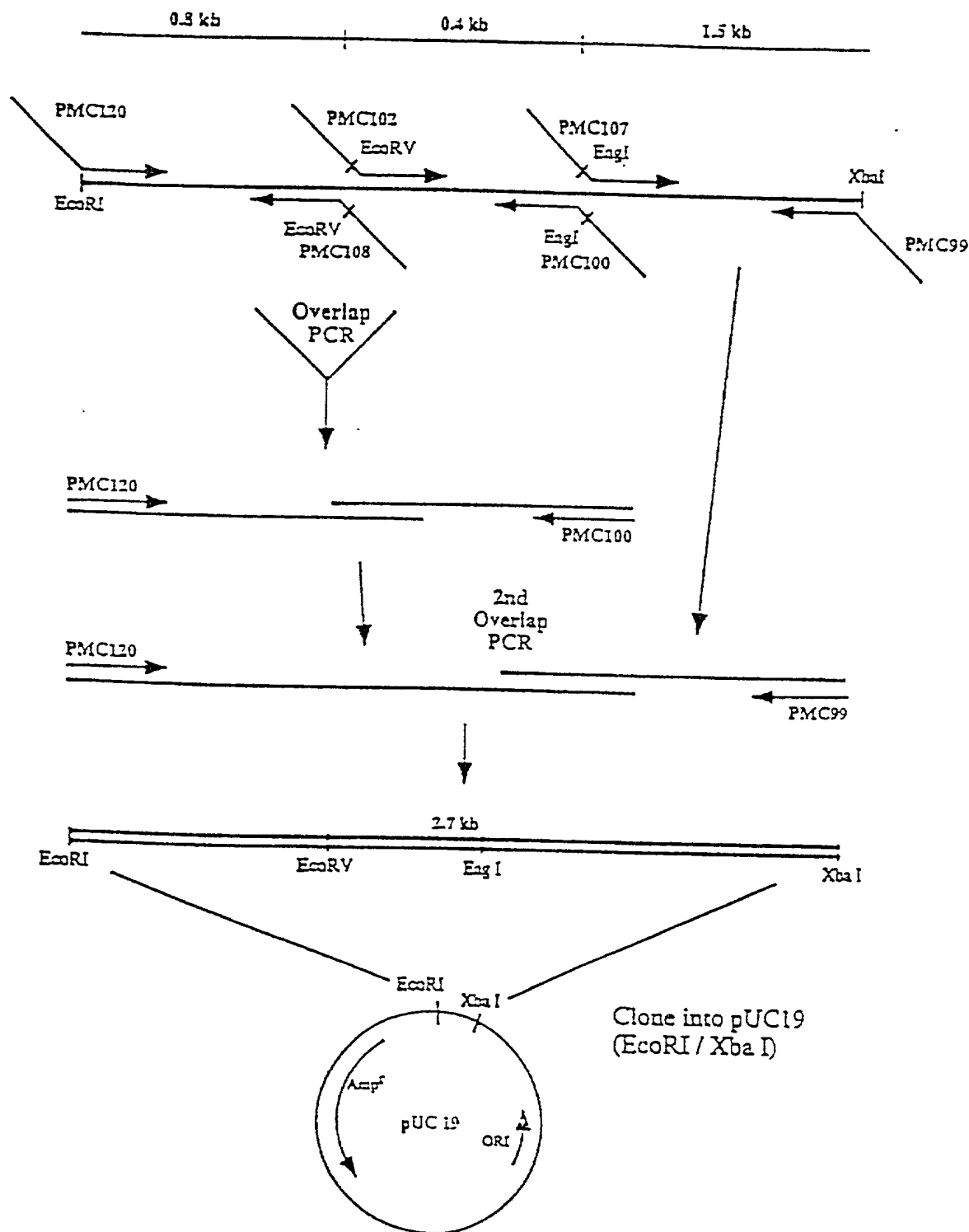
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Figure 11. The 2.7 Kb Kappa and the 1.7 Kb Heavy Chain EcoR V and Eag I Mutated Constructs



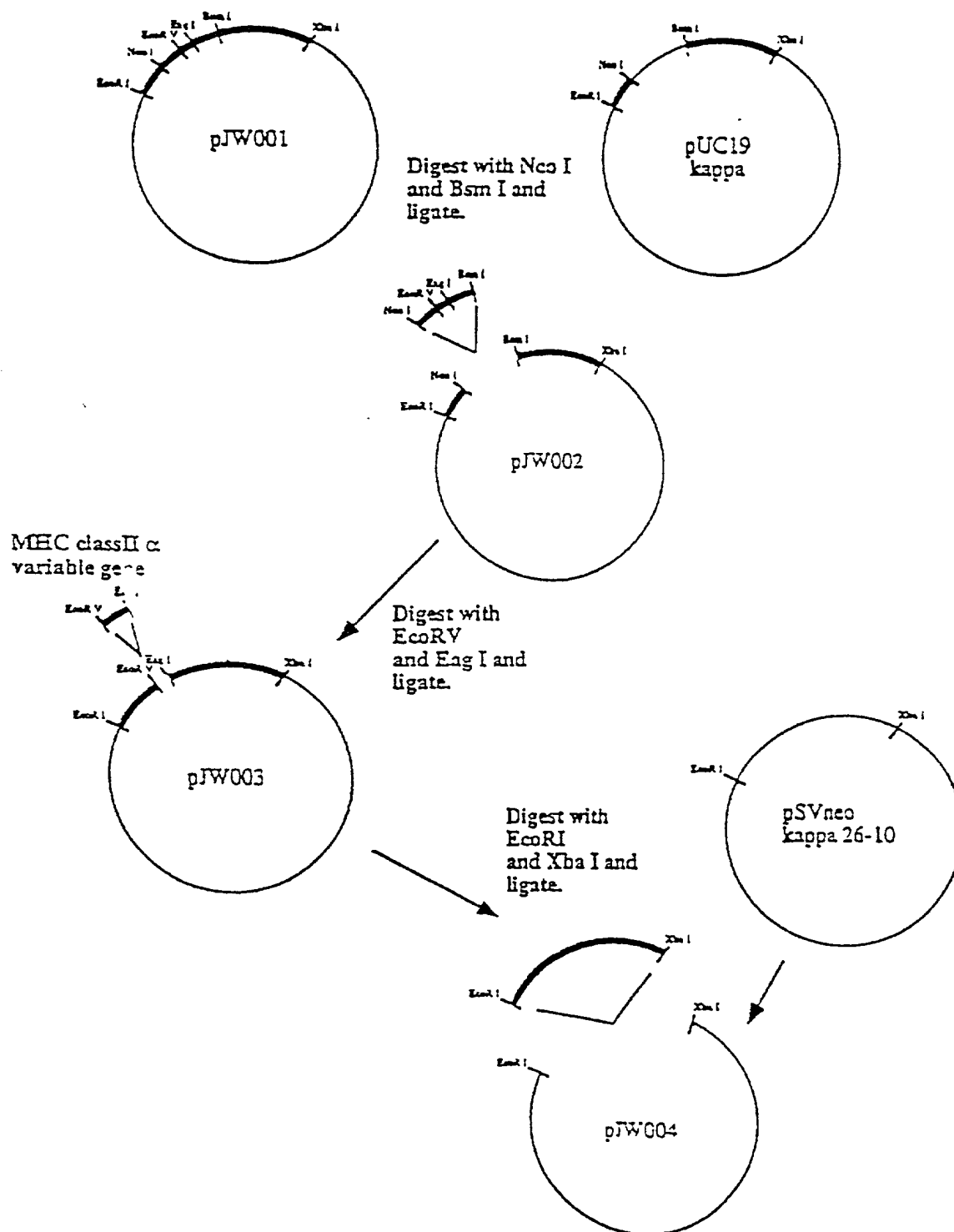
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Figure 12. PCR Site Directed Mutagenesis for Introducing EcoRV and EagI Restriction Sites into Kappa Chain 2.7kb Insert



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Figure 13. STRATEGY FOR CONSTRUCTING MHC CLASS II α / KAPPA CONSTANT GENE IN MAMMALIAN CELL EXPRESSION VECTOR



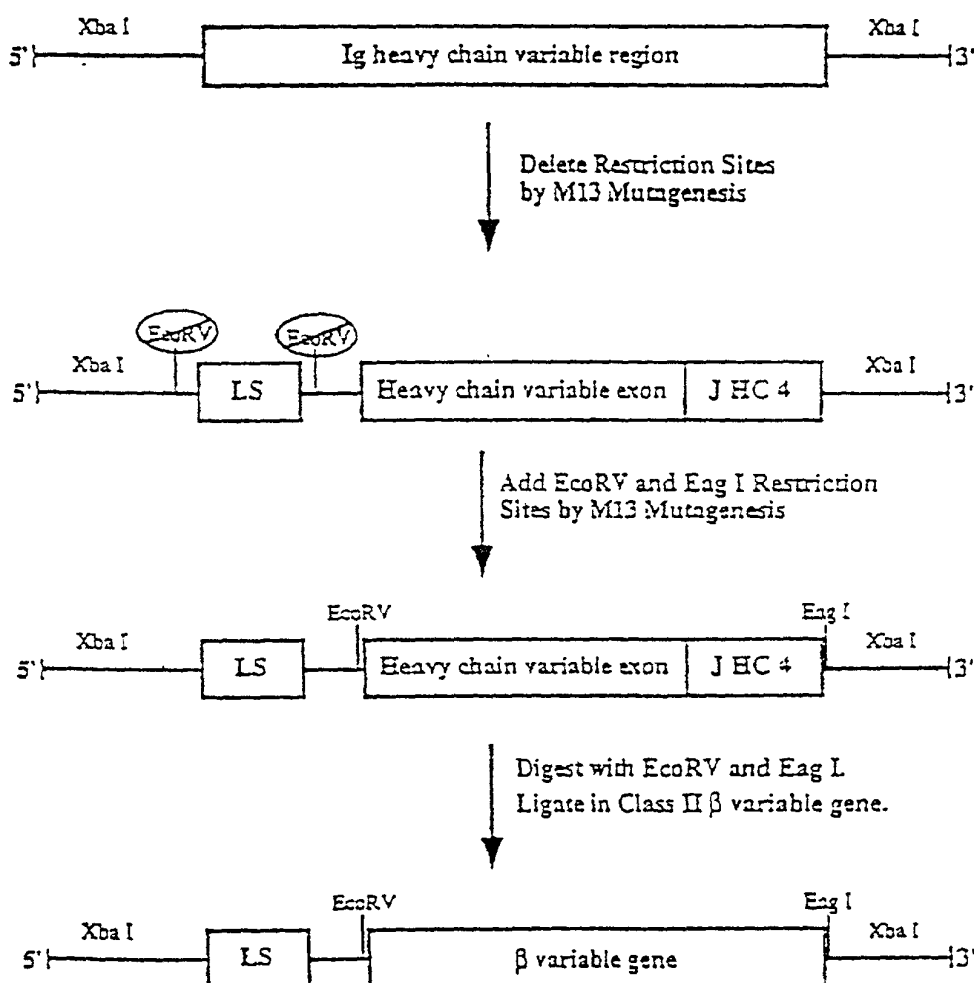
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Figure 14. Primers used for Sequencing Mutated 2.7 Kb Fragment

<u>Primer List</u>	<u>Sequence</u>
PMC-33	[5GCTCAGCTGTCTTGTTTCAGTACTGATC3']
PMC-77	[5GTAAGTAGCGGCCCG3']
PMC-111	[5GGTATGTAAAAATAAACATCACAG3']
PMC-114	[5GCTTTGCTTACGGAGTTACTG3']

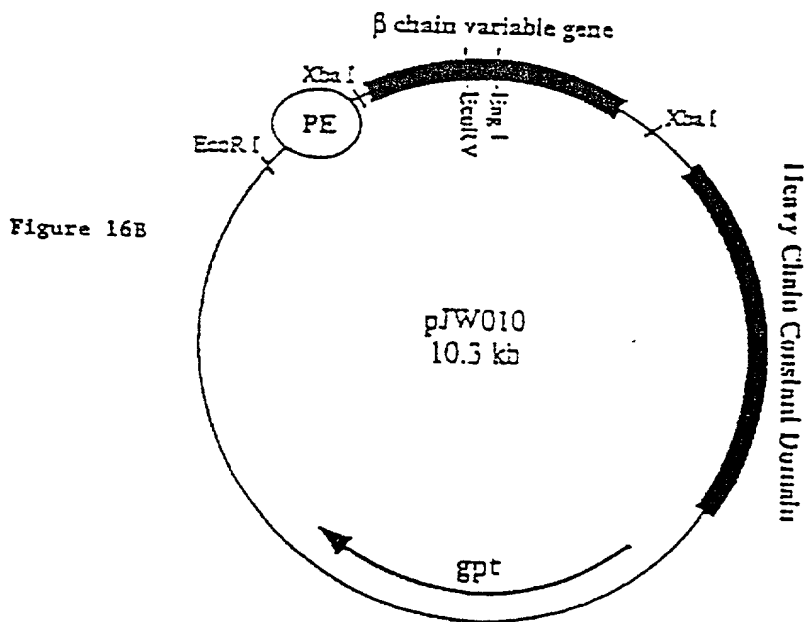
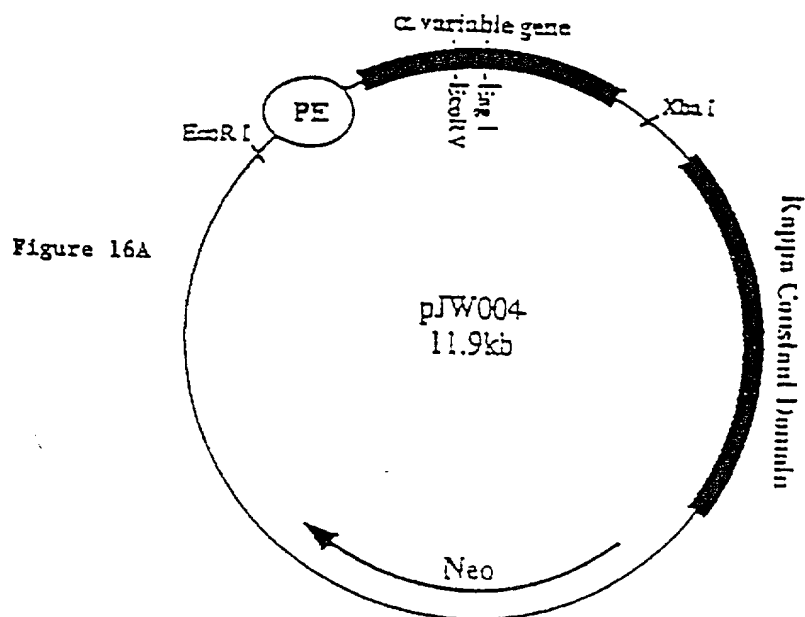
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Figure 15. Strategy for M13 Mutagenesis and Cloning of the MEC II β Variable Gene

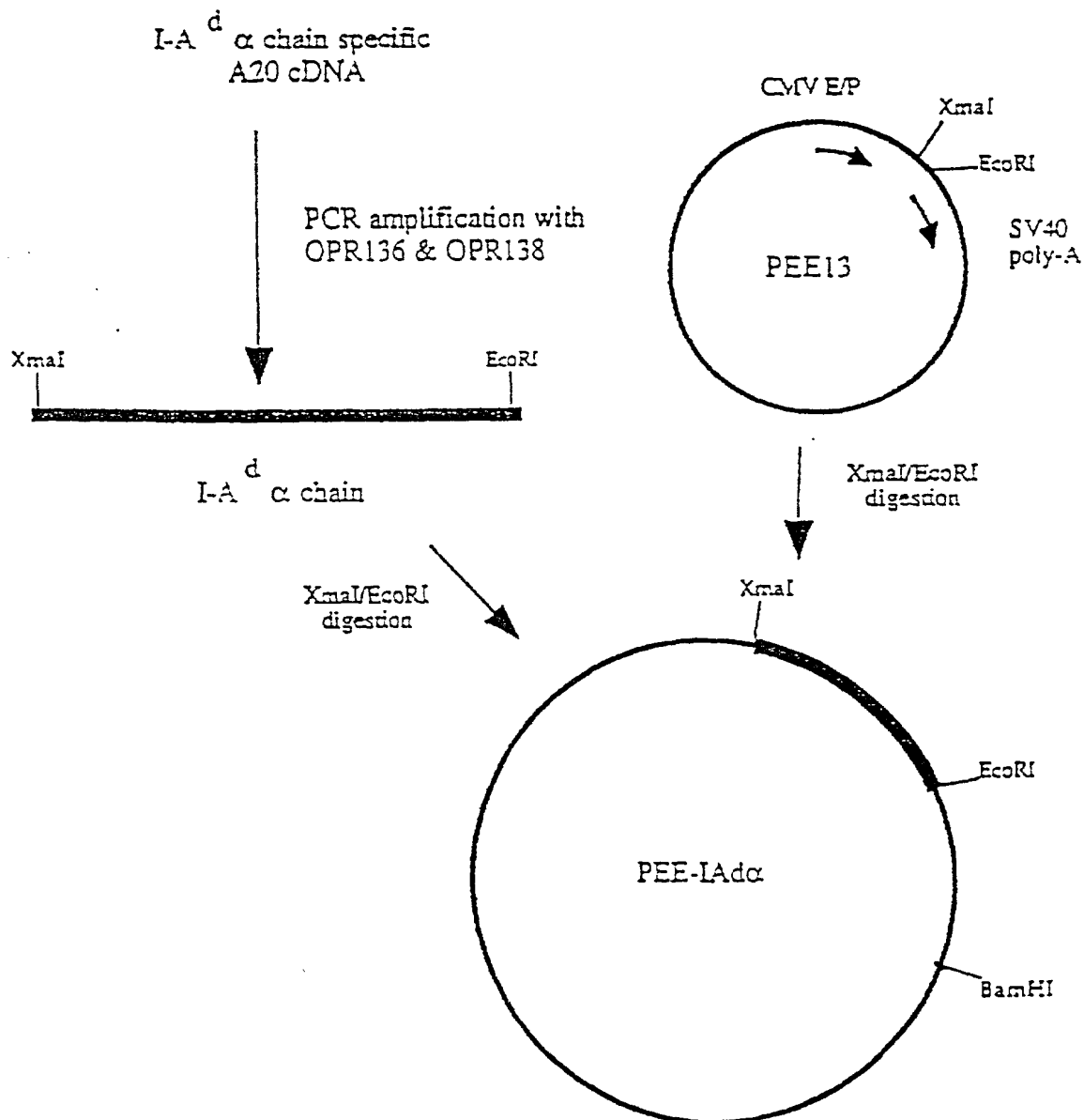
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Figure 16. Final Vectors for Expressing MEC II/ Ig Chimeric Proteins



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Figure 17 - Full length peptide linked MHC expression vectors



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Figure 17 - cont.

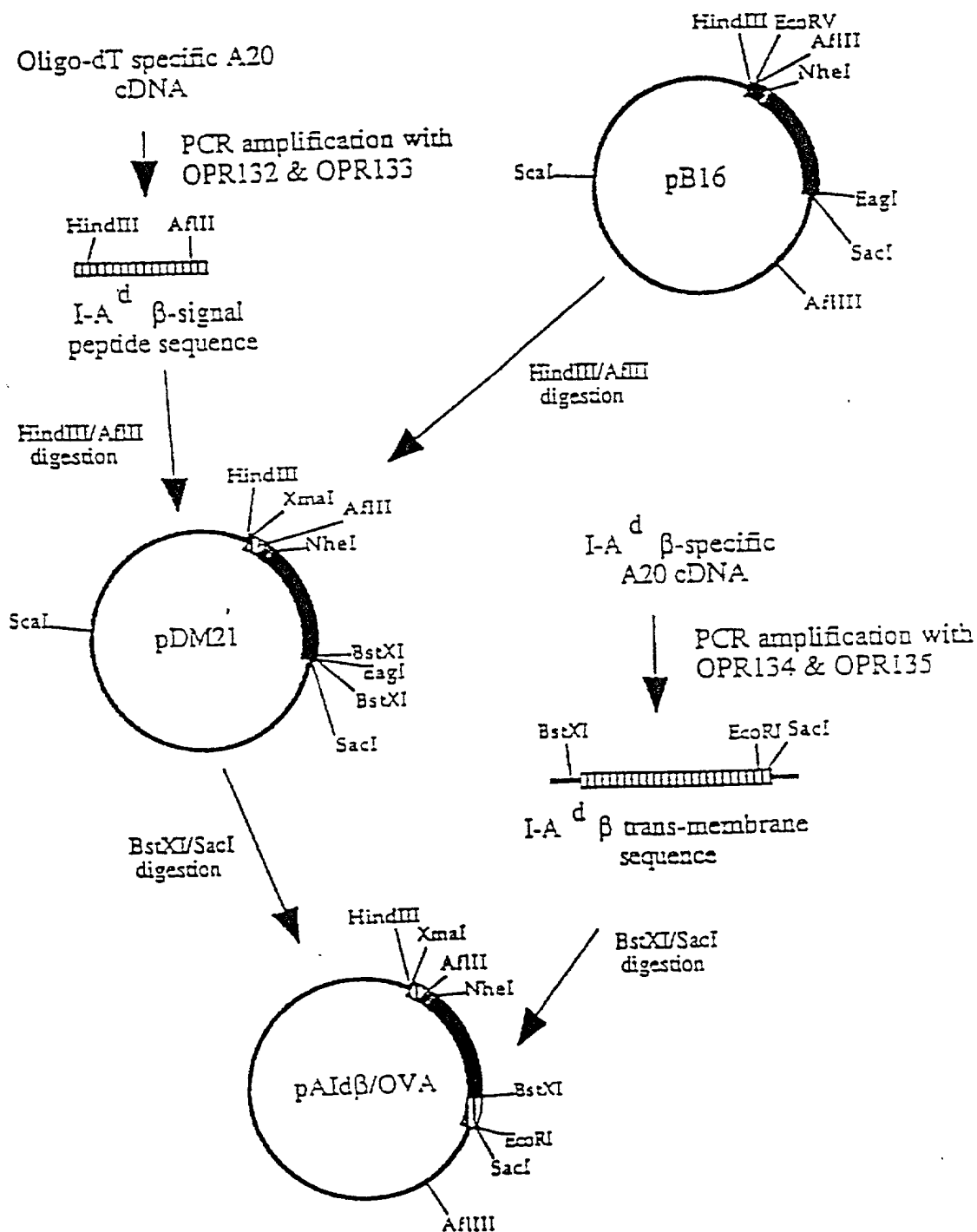
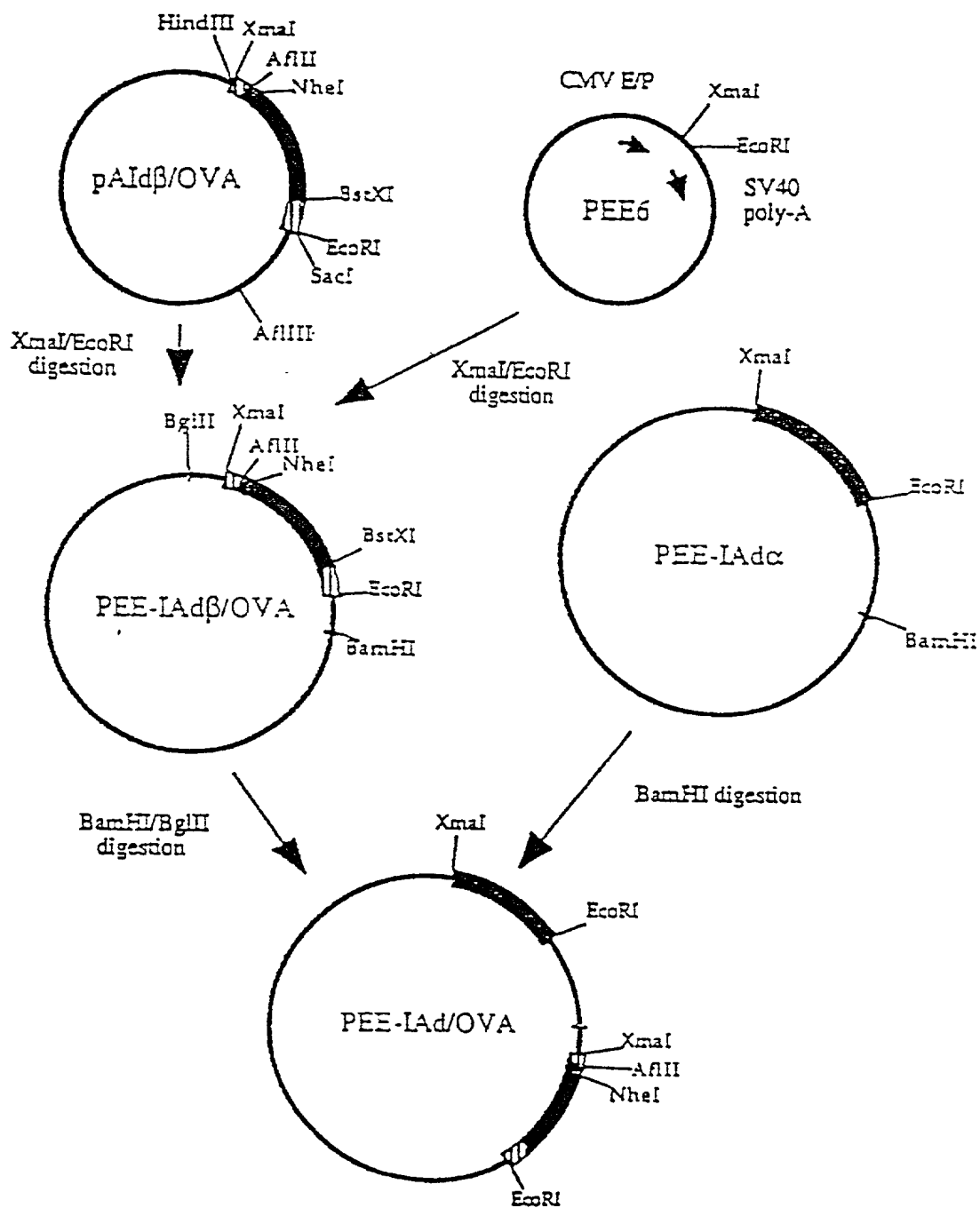


Figure 17 - cont.



```

XbaI      10          20          30          40          50
GGGGGGG C ATG GTT TGG ACC AGA GGT GTT ATT GTT GGG GTT GTT GGT
GGGGGGG C TAC GGC ACC TGG TGT GGA CAC TAA CAC GTT CAG GAG GCG
      H P C S R A L I L G V L A

      I-Ad α chain signal peptide
Kozak
consensus

      60          70          80          90
GTG AAC ACC ATG GTT ACC GTT TGG GGA GGT GAA GAG CAC ATT GAG //
GAC TTG TGG TAC GAG TGG GAG ACC GTT GAT GTT GTT TAA GTG //
L N T H L S L C G GA E Q D I E //
                               ||-1
I-Ad α chain signal peptide      Signal peptide
                                cleavage site

      750          760          770          780          EcoRI
CGA TCA GGT GGC ACC TGG AGA CAC CGA GGG GGT TTA TGA GAATTC
GCT AGT GGA GGG TGG ACC TGT GTG GGT GCG GCA AAT ACT GTTAAG
R S G G T S R H P G P L *
                               Stop
I-Ad α chain

```

```

HindIII XbaI
      10          20          30          40          50
AAGCTTCTGGG GGGGACG ATG GGT GTG CAG ATG GCG AGC GTG GTG GTG TGA GGT
TTGGAAGGGG GGGGTTC TAG CCA CAC GTC TAG GGT TCG CAG CAG CAG ACT CCA
      H A L Q I P S L L L S A

Kozak          I-A $\beta$  chain signal peptide
consensus

      60          70          80          90          100
GCT GTG GTG GTG GTG ATG GTG GTG AGC AGC CCA AGC AGC TTA AGT ATC
CCA CAC CAC CAC CAC TAG CAC CAC TCG TCG GGT TCG TCG AAT TCA TAG
      A V V V L H V L S S P R T L SA I

I-A $\beta$  chain signal peptide          signal peptide
                                   cleavage site

      110          120          130          140
TGT CAG GGT GTT CAC GGT GGT CAC GGT GAA ATC AAC GAA GGT GGT GGT
AGA GTC CCA CCA GTC CCA CCA GTC CCA GTT TAG TTG GTT CCA CCA CCA
      S Q A V H A A H A E I N E A G R

Ova peptide

      NdeI
150          160          170          180          190
GCT AGC CCA GCG GCG CCA AGT GGC CCA GCG CCA AAC TCG GAA AGC //
CCA TCG GGT GCG GCG GGT TCG GCG GGT GCG GGT TTG AGC GTT TCG //
      A S G G G C S C G G G C H S E R //

Linker region          I-A $\beta$  chain

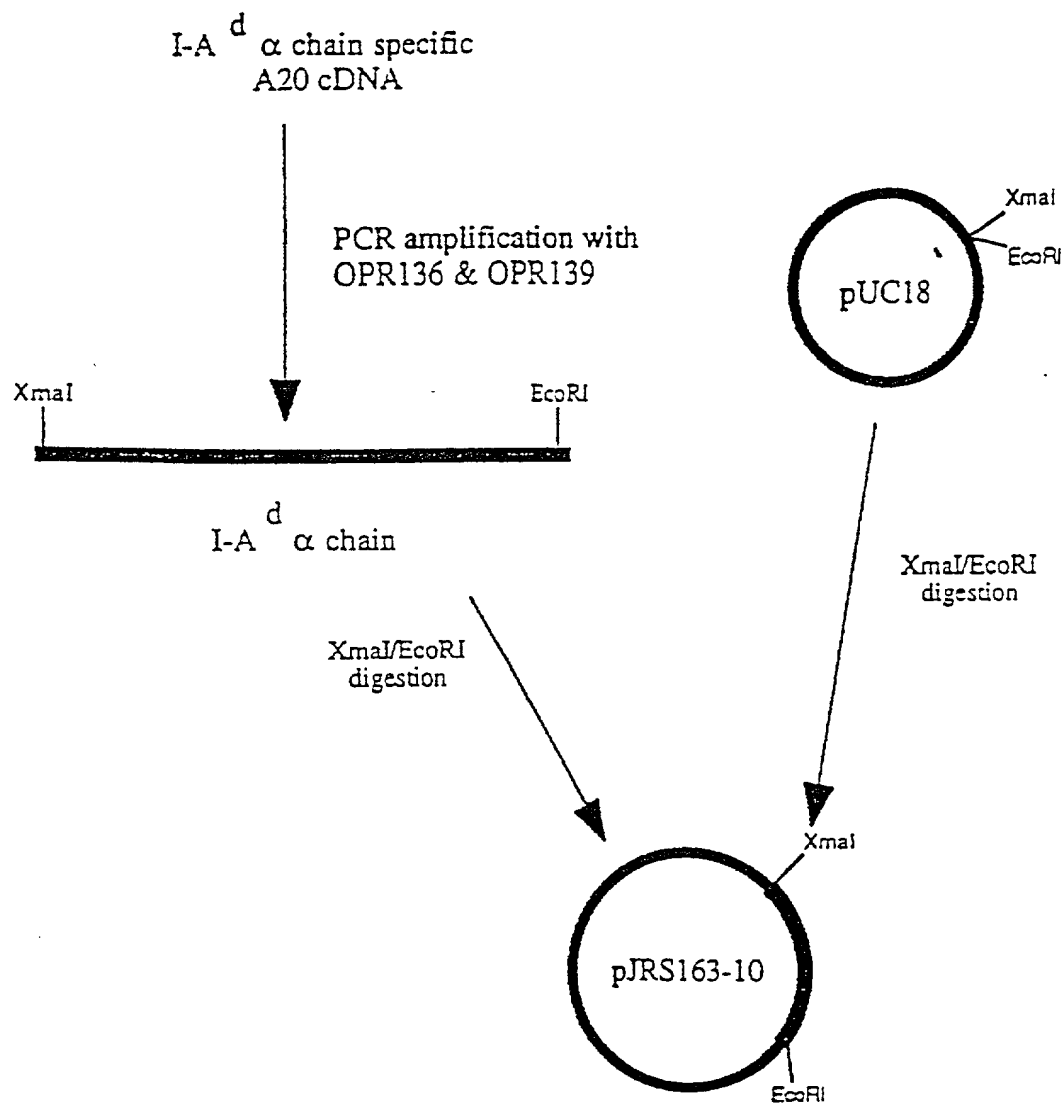
      870          880          890          900
GCT GGT CCA CCA GCG GTG GTG CAC TGA GAAT TCGAGTC
CCA CCA GGT GGT GGT CAG CAC GTC ACT CTTA TCGAGTC
      P P P A G L L Q *

I-A $\beta$  chain

```

FIGURE 19 (Sheet 1 of 7)

Full-length peptide linked MHC expression vectors



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FIGURE 19 (Sheet 2 of 7)

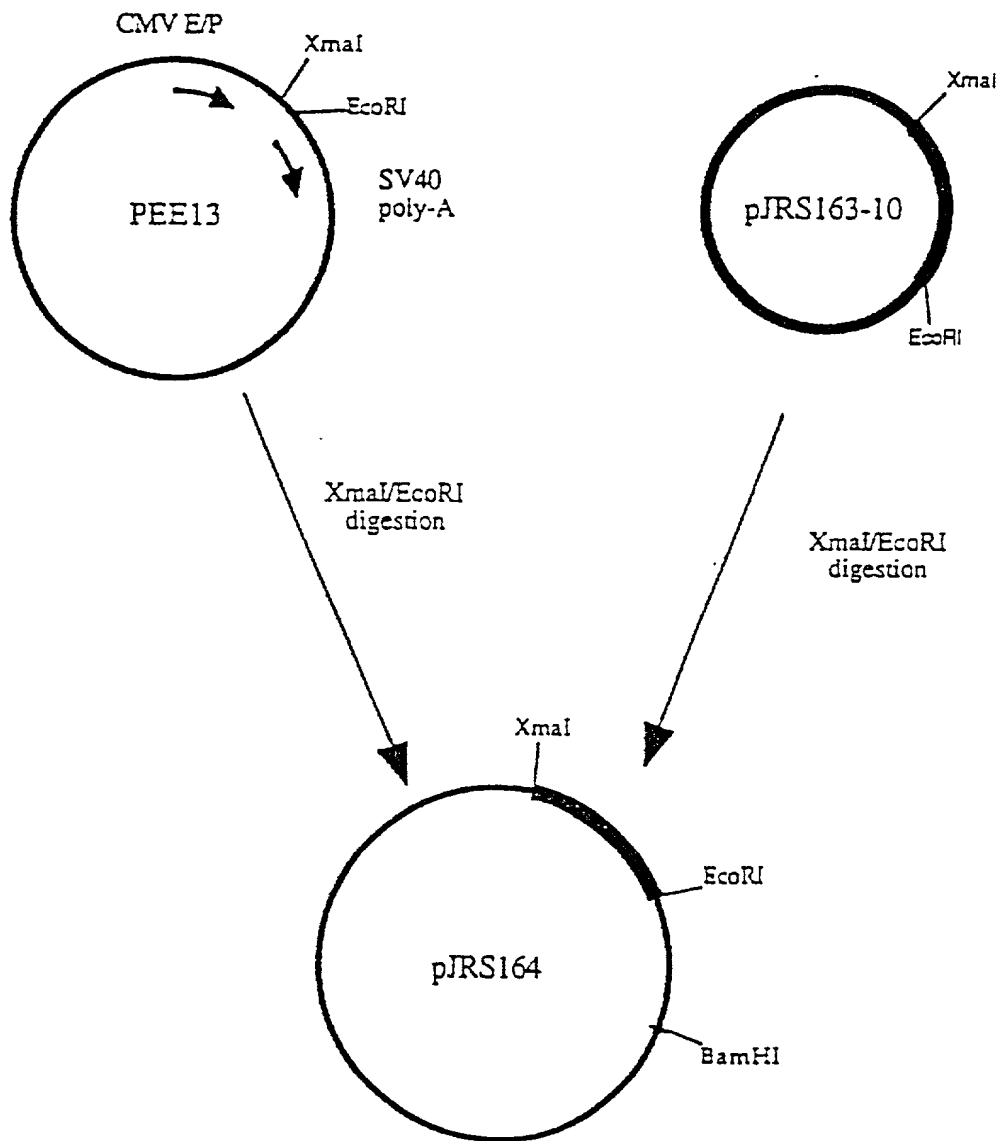
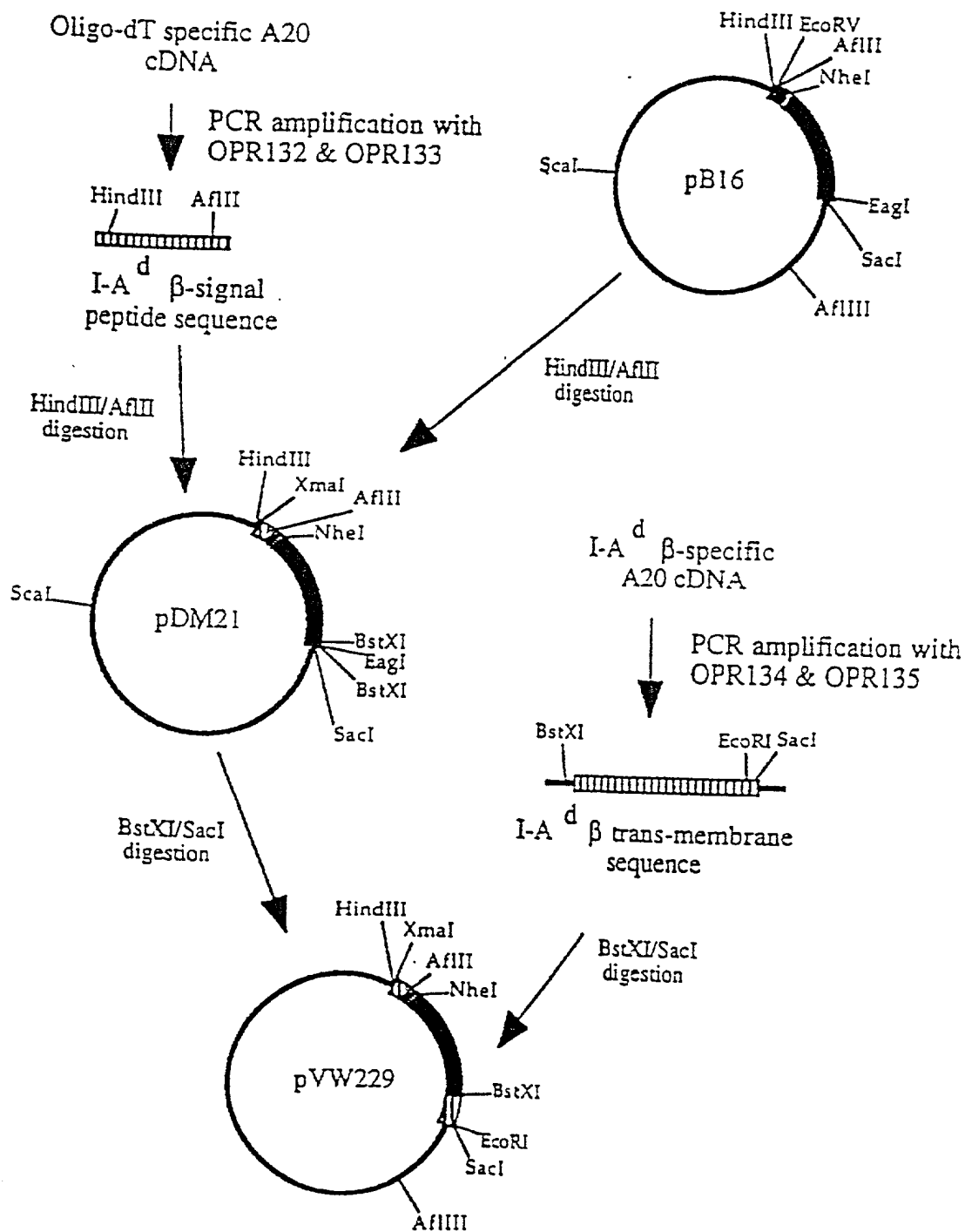
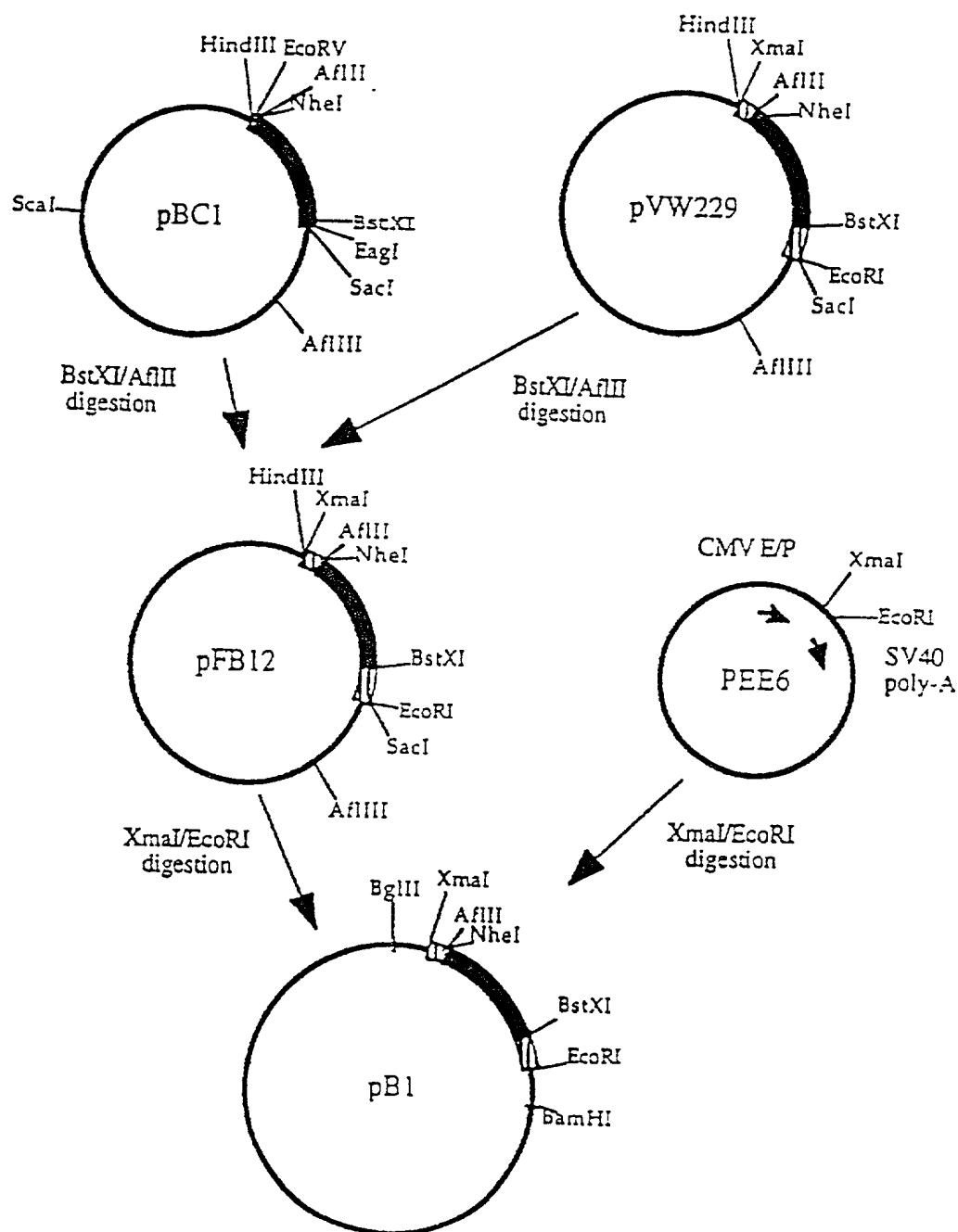


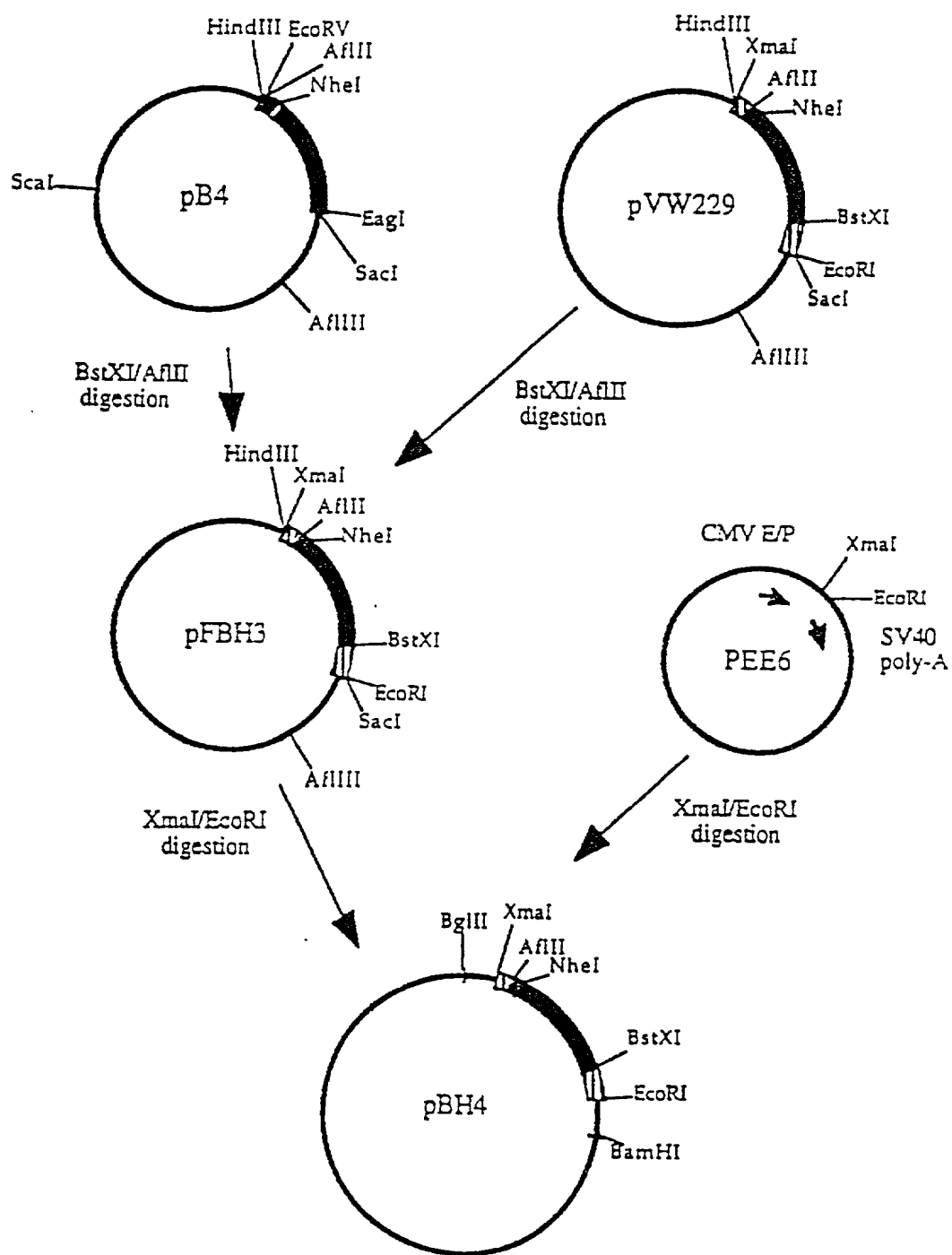
FIGURE 19 (Sheet 2 of 7)

FIGURE 19 (Sheet 3 of 7)



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FIGURE 19 (Sheet 4 of 7)



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FIGURE 19 (Sheet 6 of 7)

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FIGURE 19 (Sheet 7 of 7)

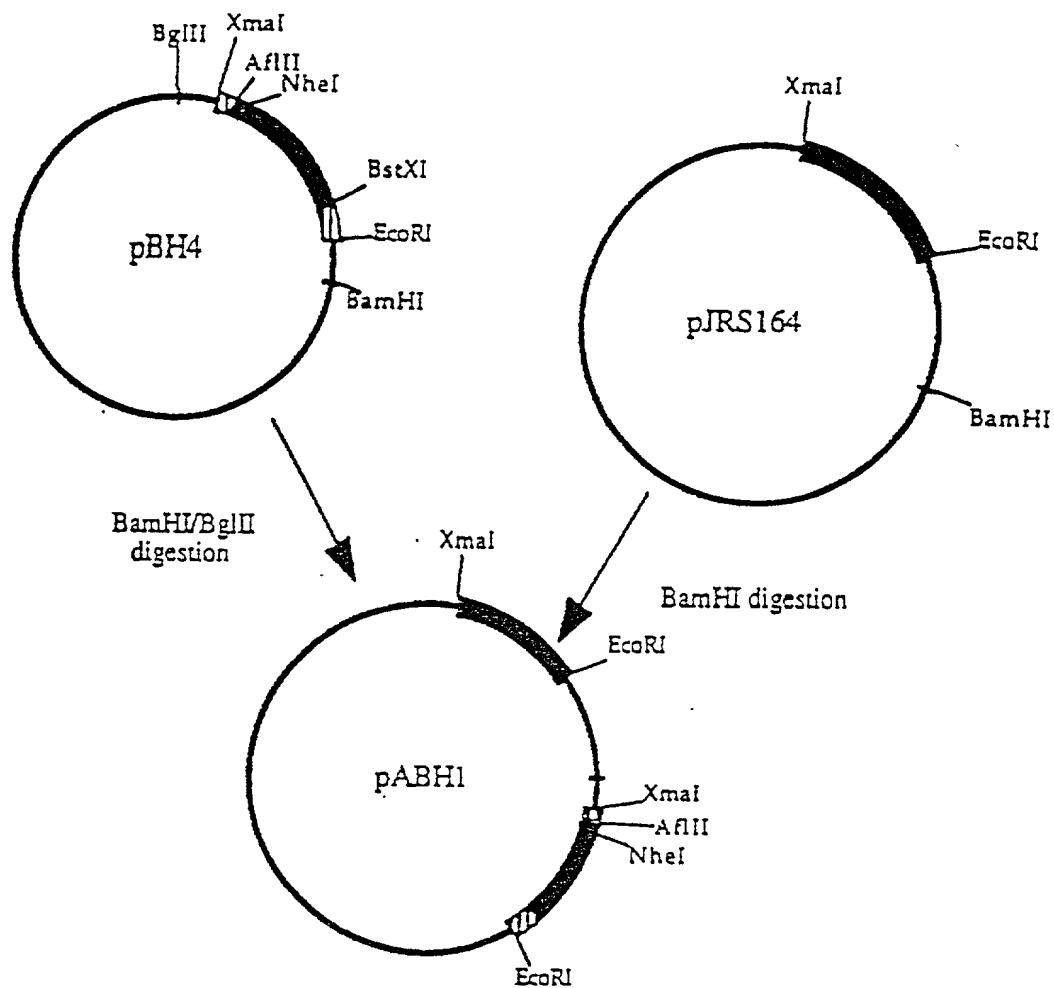


FIGURE 19 (Sheet 7 of 7)

Oligonucleotides used in cloning

I-A^d β signal peptide front primer with Kozak consensus for CellTech vector - HindIII/XmaI sites

I-A^d β signal peptide back primer with Kozak consensus for CellTech vector - AflIII site
5'-CCC CCC ACT TAA GGT CCT TGG·GCT GCT CAG CAC C-3'

I-A^d β transmembrane front primer for CellTech vector - BstXI sites
5'-CCC CCC CCA TCA CTG TGG AGT GGA GGG-3'

·I-A^d β transmembrane back primer for CellTech vector - SstI, EcoRI sites

I-A^d α signal peptide front primer with Kozak consensus for CellTech vector - HindIII/XmaI sites

I-A^d α transmembrane primer for CellTech vector - SstI/EcoRI sites

Murine B7-1 front primer with Kozak consensus for CloneTech vector - NotI site

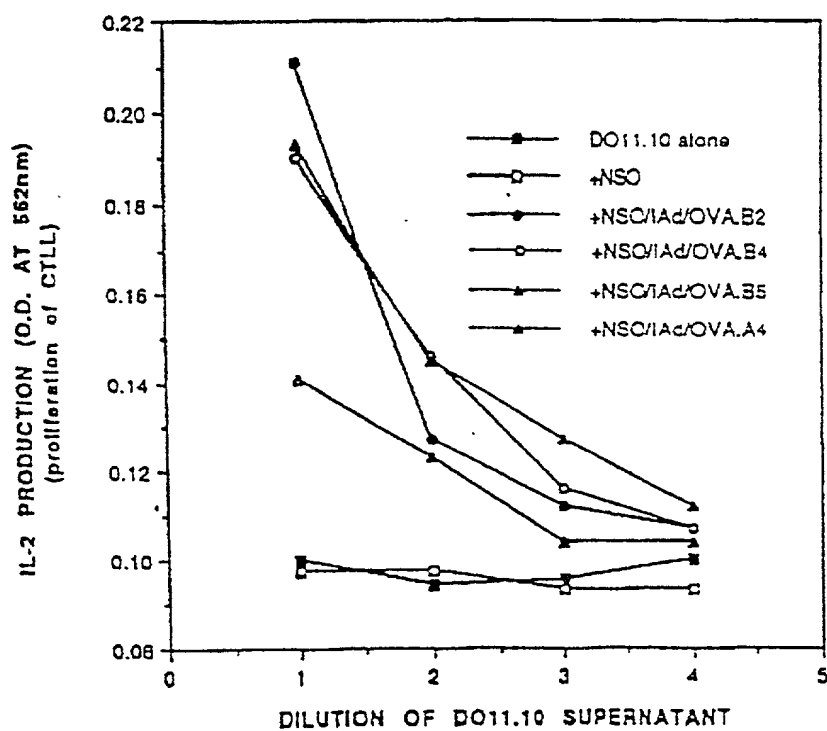
Murine B7-1 BACK primer for CloneTech vector - NotI site

5'-CCC CCC GCG GCC GCT TTA AAA ACA TGT ATC ACT TTT-3'

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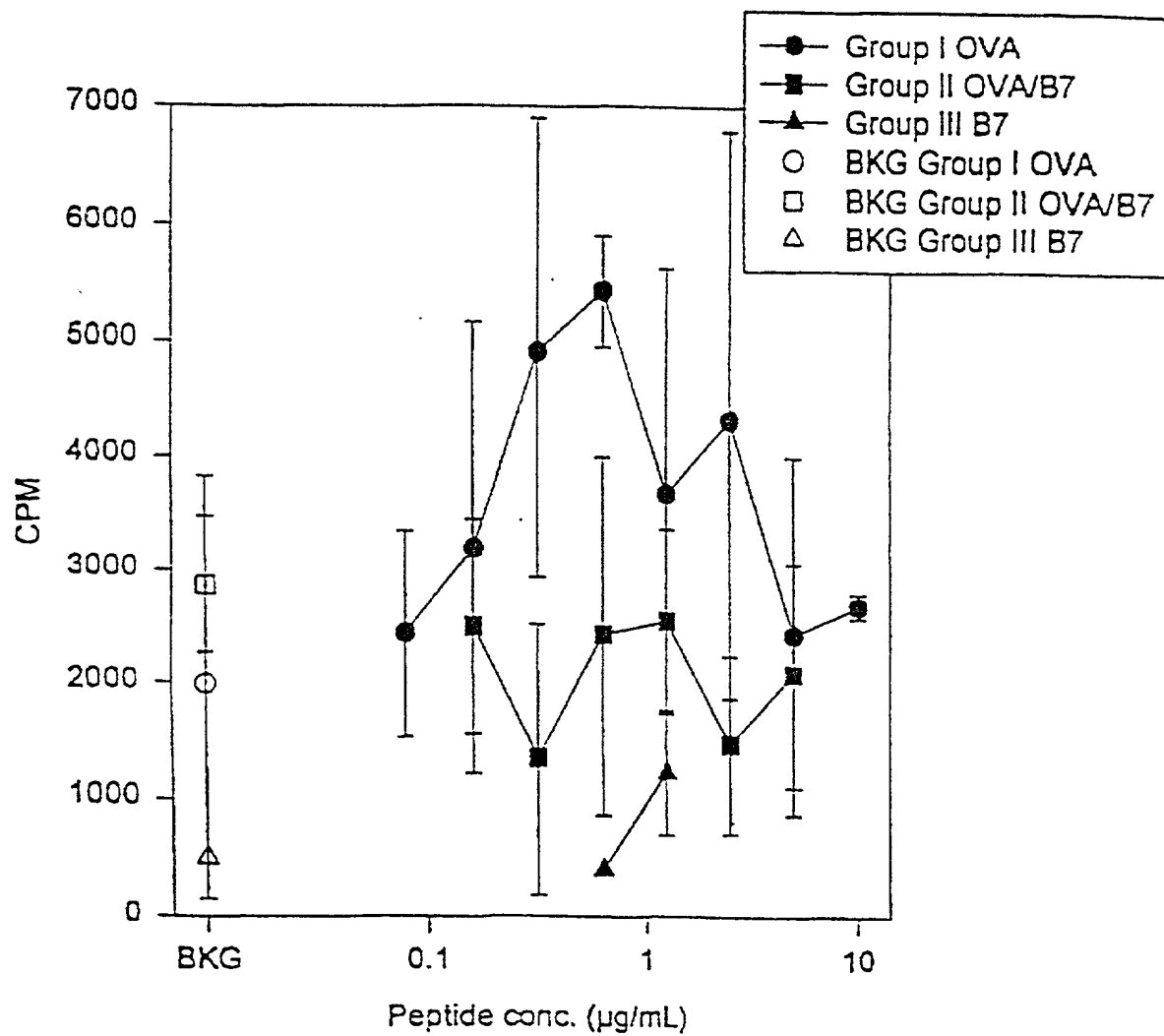
FIGURE 21

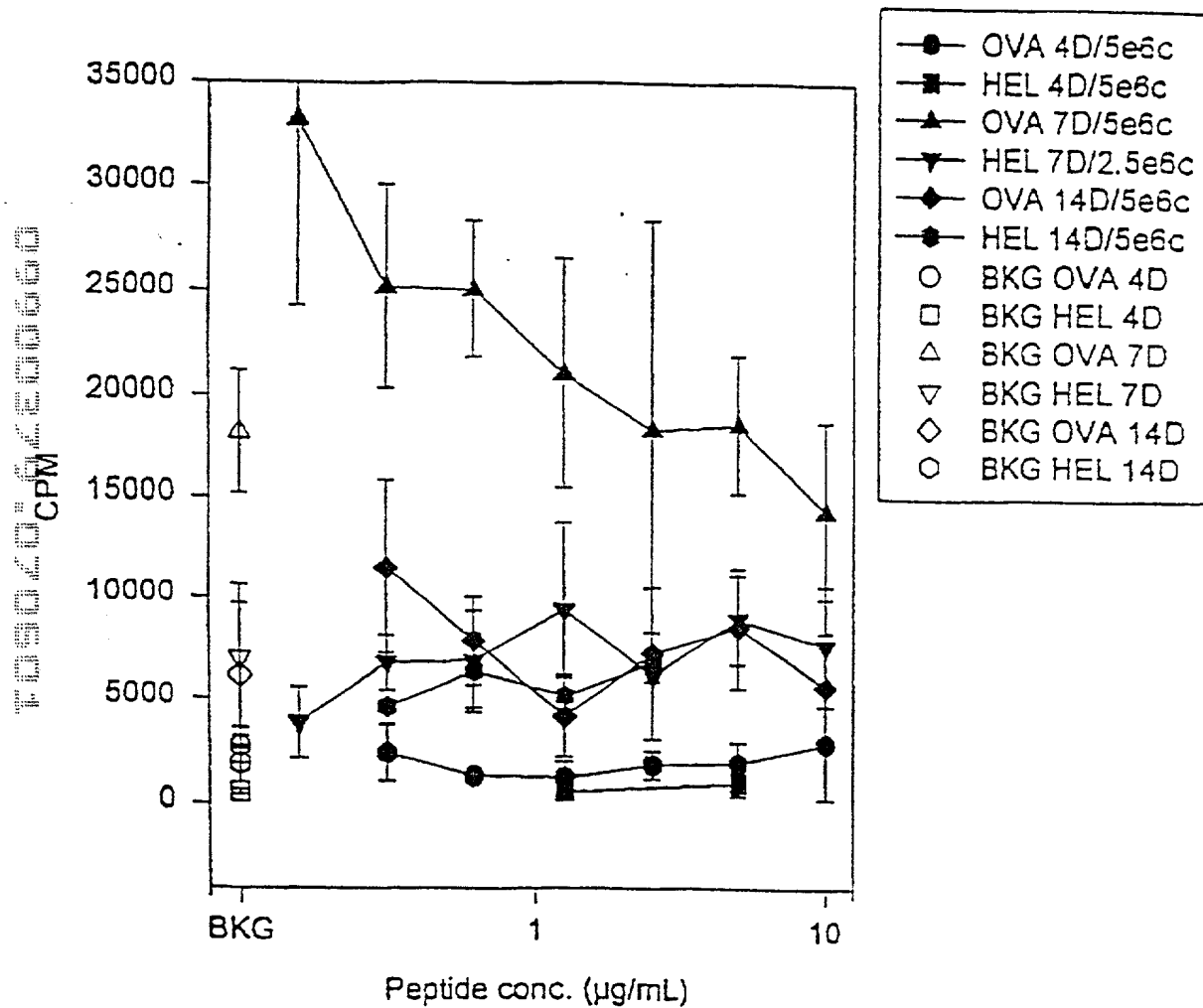
NSO/ClassII/OVA clones Stimulate IL-2 Production from DO11.10



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FIGURE 22

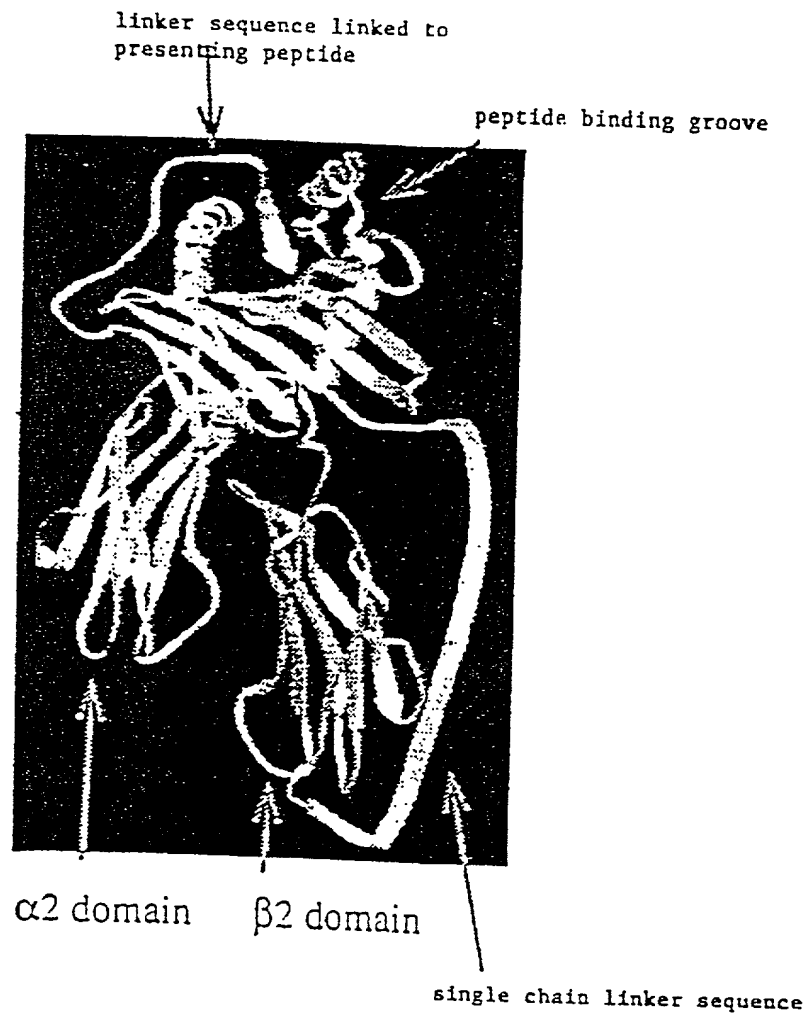
INTRAMUSCULAR IAd/OVA & B7 DNA INJECTIONS PROLIFERATION ASSAY



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FIGURE 23**INTRADERMAL IAd/OVA & IAd/HEL DNA INJECTIONS
PROLIFERATION ASSAY
4, 7 & 14 DAYS POST INJECTION**

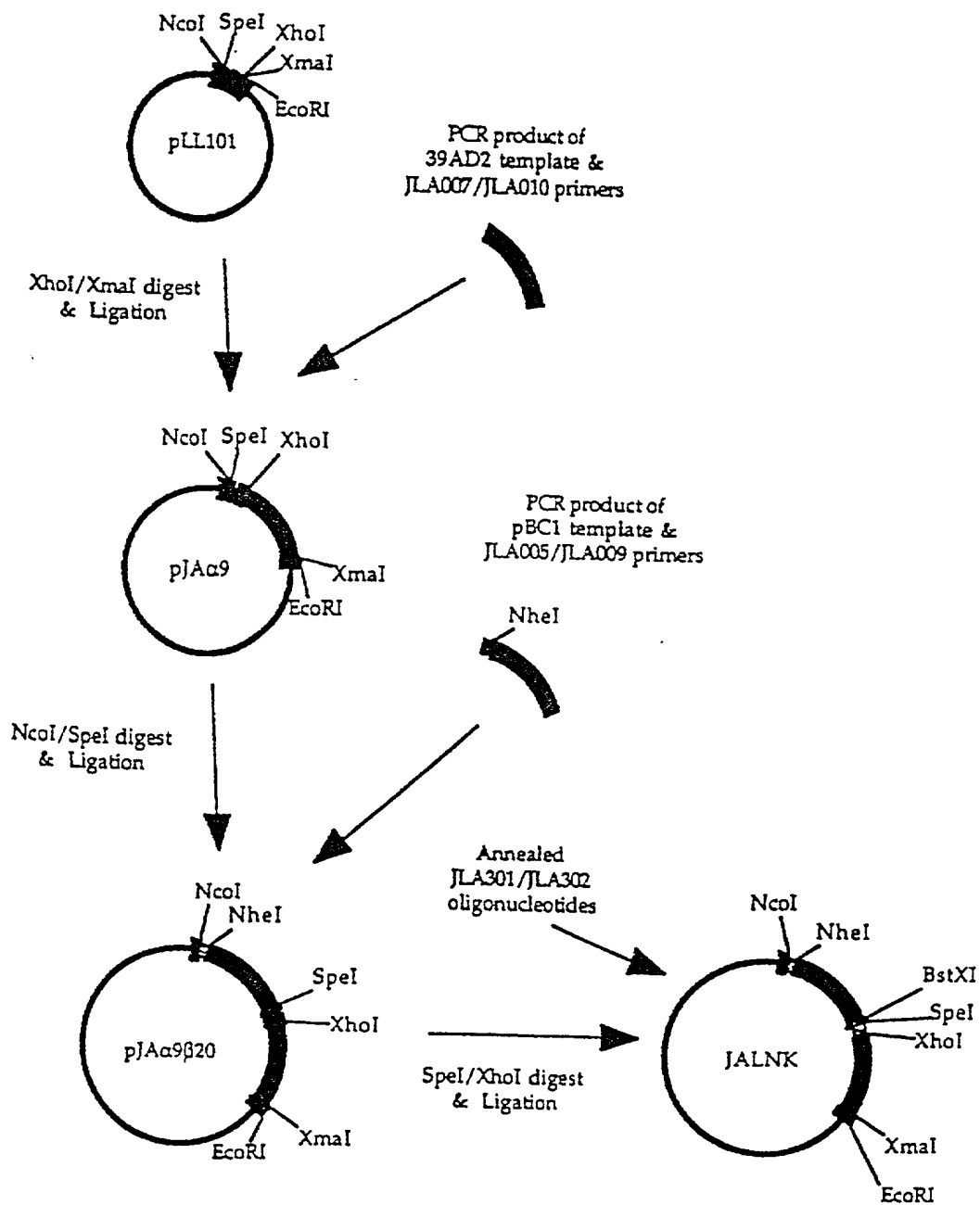
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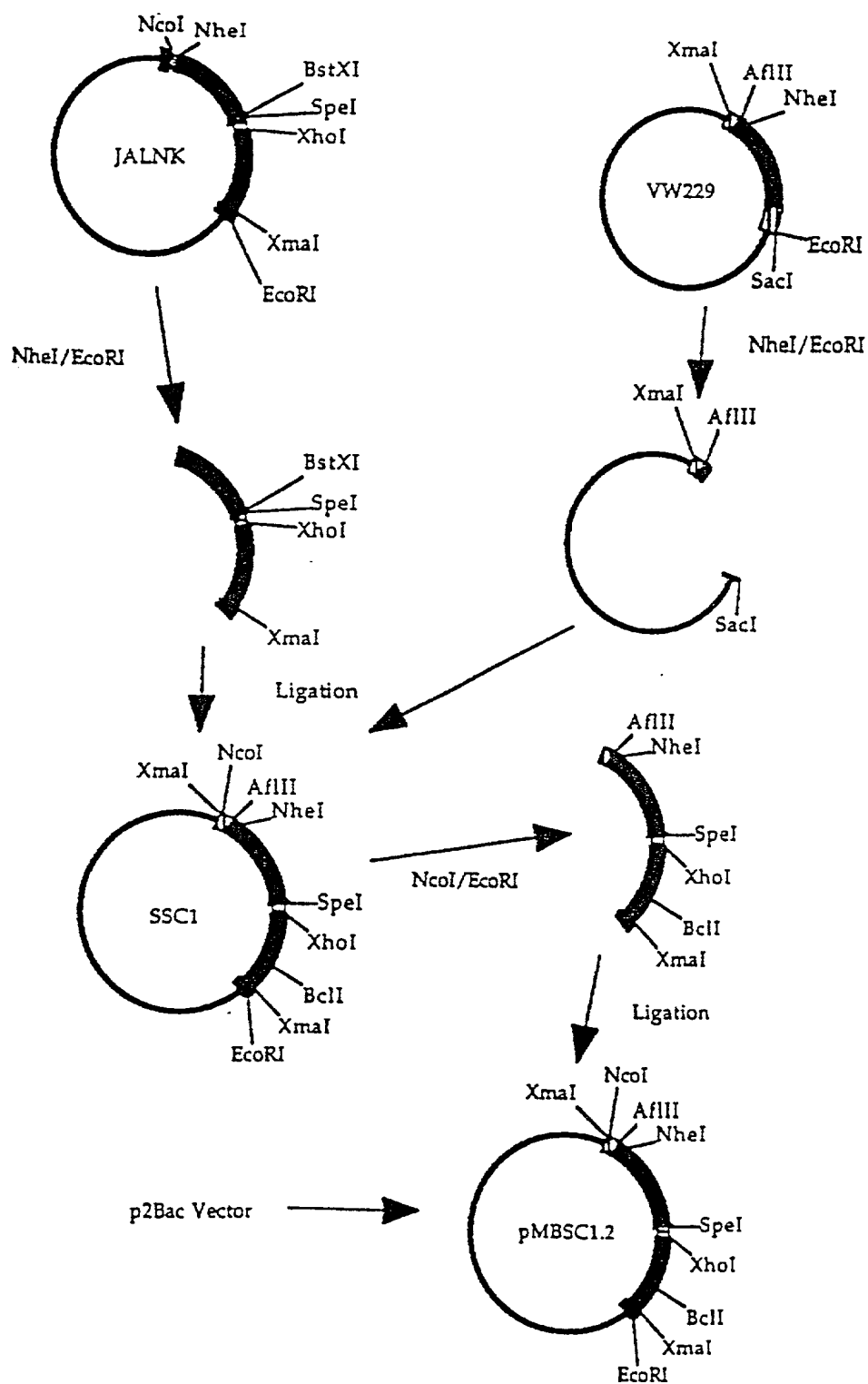
FIGURE 24

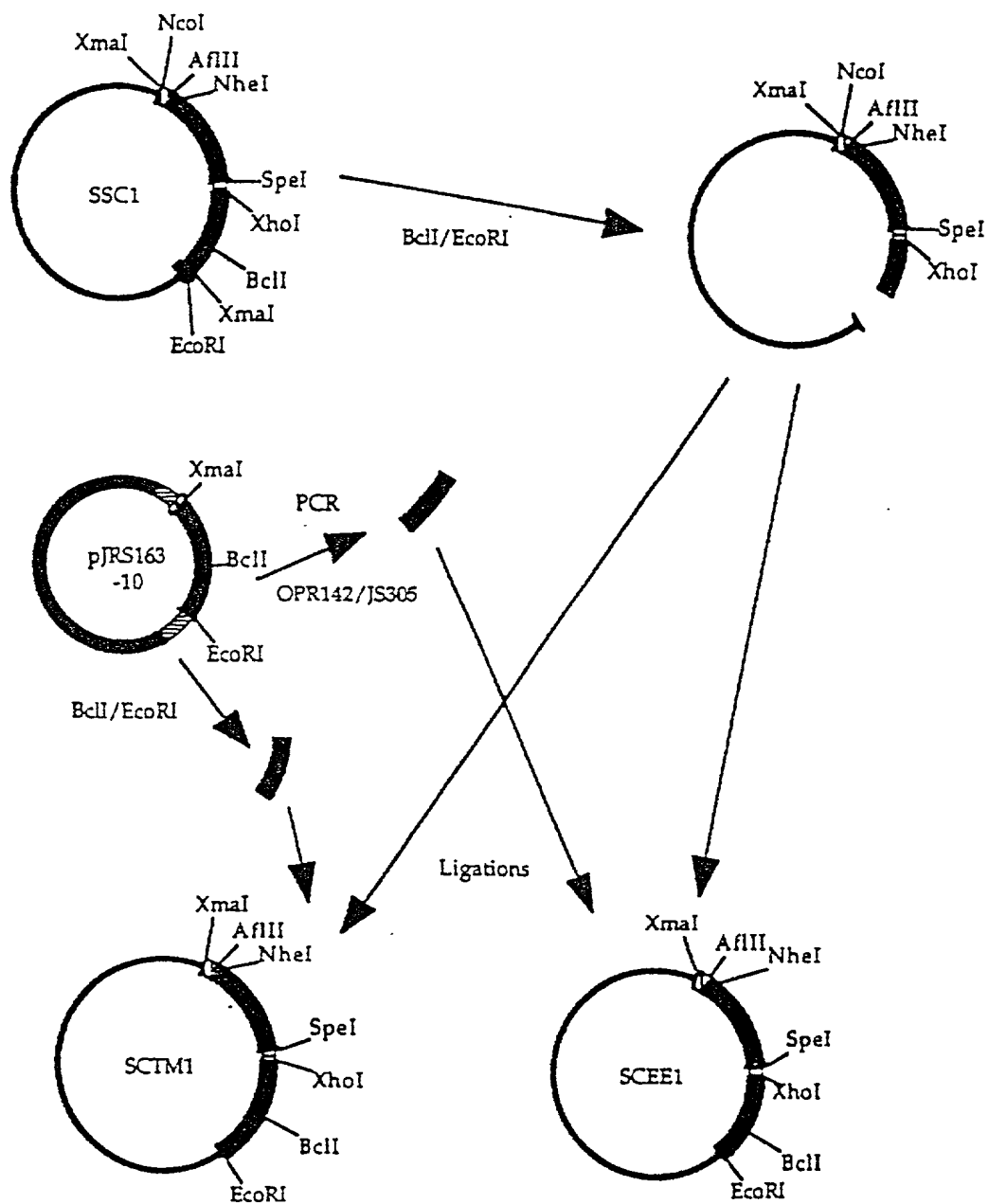


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FIGURE 25 (SHEET 1 OF 4)

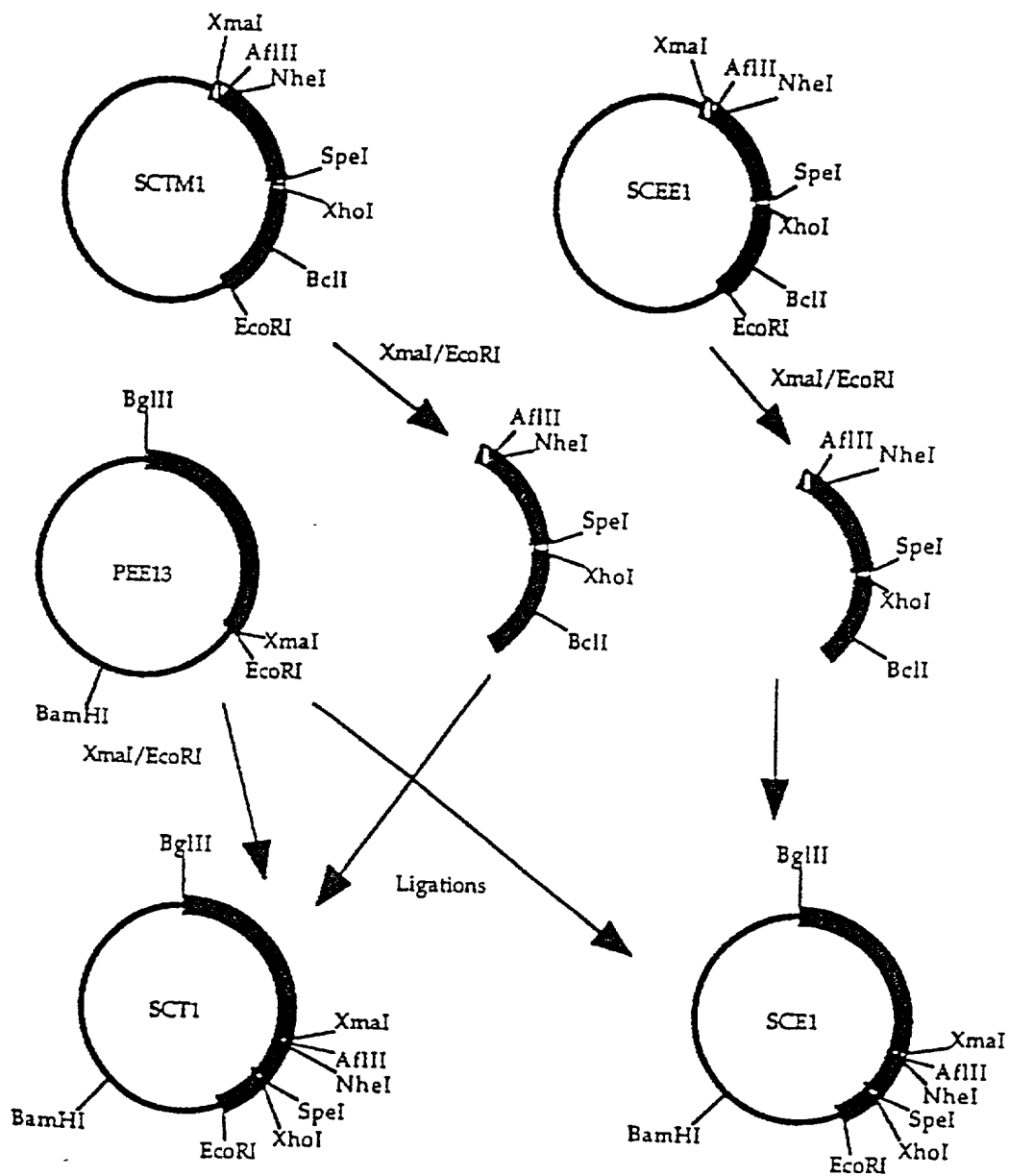


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FIGURE 25 (SHEET 2 OF 4)

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FIGURE 25 (SHEET 3 OF 4)

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FIGURE 25 (SHEET 4 OF 4)



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FIGURE 26

JLA-005

5' -CCCCCGCCATGGCCGCTAGCGGAGGGGGCGGAAGC-3'

JLA-007

5' -CCCGGGGCGCTCGAGTGAAGACGACATTGAGGCCGAC-3'

JLA-009

5' -CCCCCACTAGTCCACTCCACAGTGATGGGGCT-3'

JLA-010

5' -CCCCCCCCCGGGACCAGTGTTTCAGAACCGGCTCCTC-3'

JLA-301

5' -TCGAGGAACCGCCACCGCCAGAACCGCCGCCACCGGA-
ACCACCACCGCCGCTGCCACCGCCACCA-3'

JLA-302

5' -CTAGTGGTGGCGGTGGCAGCGGCGGTGGTGGTTCCGG-
TGGCGGCGGTTCTGGCGGTGGCGGTTC-3'

OPR-142

5' -CTTGGAATCTTGACTAAGAGG-3'

JS-305

5' -CAGGTCGAATTCTCATTCATCGGCATGTACTCTTCTT-
CCTCCCAGTGTTTCAGAACCGG-3'

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FIGURE 27 (SHEET 1 OF 4)

```

      10      20      30      40      50
      *      *      *      *      *
CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG
GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC
      M  A  L  Q  I  P  S  L  L  L  S  A  A  V  V>
<----- I-Ad β chain leader ----->

      60      70      80      90
      *      *      *      *
GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
      V  L  M  V  L  S  S  P  R  T  L  S  I  S  Q  A>
----->-----<-----

100      110      120      130      140
      *      *      *      *      *
GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT
      V  H  A  A  H  A  E  I  N  E  A  G  R  A  S  G>
----- OVA 323-339 ----->-----<-----

150      160      170      180      190
      *      *      *      *      *
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
      G  G  G  S  G  G  G  G  N  S  E  R  H  F  V  V>
-- 10 amino acid linker -->----- I-Ad β-1 domain -----<-----

200      210      220      230      240
      *      *      *      *      *
CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC
      Q  F  K  G  E  C  Y  Y  T  N  G  T  Q  R  I  R>
----->-----<-----

250      260      270      280      290
      *      *      *      *      *
CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTC
      L  V  T  R  Y  I  Y  N  R  E  E  Y  V  R  Y  D>
----->-----<-----

300      310      320      330
      *      *      *      *
AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG
      S  D  V  G  E  Y  R  A  V  T  E  L  G  R  P  D>
----->-----<-----

340      350      360      370      380
      *      *      *      *      *
GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC
CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TGC GCC CGG
      A  E  Y  W  N  S  Q  P  E  I  L  E  R  T  R  A>
----->-----<-----

```

FIGURE 27 (SHEET 1 OF 4)

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FIGURE 27 (SHEET 2 OF 4)

```

390      400      410      420      430
*      *      *      *      *
GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC
CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG
E V D T A C R H N Y E G P E T S>
-----

440      450      460      470      480
*      *      *      *      *
ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC
TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CGG TAG AGG GAC AGG
T S L R R L E Q P N V A I S L S>
--- I-Ad β-1 domain -><----- I-Ad β-2 domain -----

490      500      510      520      530
*      *      *      *      *
AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA
TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT
R T E A L N H H N T L V C S V T>
-----

540      550      560      570
*      *      *      *
GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG
CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC
D F Y P A K I K V R W F R N G Q>
-----

580      590      600      610      620
*      *      *      *      *
GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC
CTC CTC TGT CAC CCC CAG ACT AGG TGT GTC GAA TAA TCC TTA CCC CTG
E E T V G V S S T Q L I R N G D>
-----

630      640      650      660      670
*      *      *      *      *
TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA
ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT
W T F Q V L V M L E M T P H Q G>
-----

680      690      700      710      720
*      *      *      *      *
GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC
CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GGG TAG
E V Y T C H V E H P S L K S P I>
----- I-Ad β-2 domain -----

730      740      750      760      770
*      *      *      *      *
ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC
TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG
T V E W T S G G G G S G G G G S>
-----><----- 24 amino acid linker -----

```

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FIGURE 27 (SHEET 3 OF 4)

```

      780      790      800      810
      *      *      *      *
GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCC AGT GAA GAC GAC ATT
CCA CCG CCG CCA AGA CCG CCA CCG CCA AGG AGC TCA CTT CTG CTG TAA
G  G  G  G  S  G  G  G  G  S  S  S  E  D  D  I>
----->-----<-----

820      830      840      850      860
      *      *      *      *      *
GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT
CTC CCG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA
E  A  D  H  V  G  F  Y  G  T  T  V  Y  Q  S  P>
----- I-Ad α-1 domain -----

870      880      890      900      910
      *      *      *      *      *
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC
CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG
G  D  I  G  Q  Y  T  H  E  F  D  G  D  E  L  F>
-----

920      930      940      950      960
      *      *      *      *      *
TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT
ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA
Y  V  D  L  D  K  K  K  T  V  W  R  L  P  E  F>
-----

970      980      990      1000      1010
      *      *      *      *      *
GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT
CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA
G  Q  L  I  L  F  E  P  Q  G  G  L  Q  N  I  A>
-----

1020      1030      1040      1050
      *      *      *      *
GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC
CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG
A  E  K  H  N  L  G  I  L  T  K  R  S  N  F  T>
----- I-Ad α-1 domain -----

1060      1070      1080      1090      1100
      *      *      *      *      *
CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT
GGT CGA TGG TTA CTC CGA GGA GTT CCG TGA CAC AAG GGG TTC AGG GGA
P  A  T  N  E  A  P  Q  A  T  V  F  P  K  S  P>
----->----- I-Ad α-2 domain -----

1110      1120      1130      1140      1150
      *      *      *      *      *
GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC
CAC GAC GAC CCA GTC GCG TTG TCG GAA TAG ACG AAA CAC CTG TTG TAG
V  L  L  G  Q  P  N  T  L  I  C  F  V  D  N  I>
-----

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FIGURE 27 (SHEET 4 OF 4)

1160	1170	1180	1190	1200
<p>TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC AAG GGT GGA CAC TAG TTG TAG TGT ACC GAG TCT TTA TCG TTC AGT CAG F P P V I N I T W L R N S R S V></p>				

1210	1220	1230	1240	1250
<p>ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG T D G V Y E T S F L V N R D E S></p>				

1260	1270	1280	1290	
<p>TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT AAG GTG TTC GAC ACA ATA GAG TGG AAG TAG CGA ACA CTA CTA CTG TAA F H K L S Y L T F I P S D D D I></p>				

1300	1310	1320	1330	1340
<p>TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTT Y D C K V E H W G L E E P V L K></p>				
----- I-Ad α -2 domain -----				
1350	1360	1370	1380	
<p>CAC TGG TCC CGG GCT AGT CAC CAT CAC CAT CAT CAC TAG GTG ACC AGG GCC CGA TCA GTG GTA GTG GTA GTA GTG ATC H W S R A S H H H H H H *></p>				
-----><----- 6 X HIS tag ----->				

FIGURE 27 (SHEET 4 OF 4)

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FIGURE 28 (SHEET 1 OF 4)

```

      10      20      30      40      50
      *      *      *      *      *
CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG
GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC
      M  A  L  Q  I  P  S  L  L  L  S  A  A  V  V>
<----- I-Ad β chain leader ----->

      60      70      80      90
      *      *      *      *
GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
      V  L  M  V  L  S  S  P  R  T  L  S  I  S  Q  A>
----->-----<-----

    100      110      120      130      140
    *      *      *      *      *
GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
CAA GTG CGA CGA GTG CGA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT
      V  H  A  A  H  A  E  I  N  E  A  G  R  A  S  G>
----- OVA 323-339 ----->-----<-----

    150      160      170      180      190
    *      *      *      *      *
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
      G  G  G  S  G  G  G  G  N  S  E  R  H  F  V  V>
-- 10 amino acid linker -->----- I-Ad β-1 domain -----<-----

    200      210      220      230      240
    *      *      *      *      *
CAG ATC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TCC GTC CGC TAT GCC
      Q  F  K  G  E  C  Y  Y  T  N  G  T  Q  R  I  R>
----->-----<-----

    250      260      270      280      290
    *      *      *      *      *
CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG
      L  V  T  R  Y  I  Y  N  R  E  E  Y  V  R  Y  D>
----->-----<-----

    300      310      320      330
    *      *      *      *
AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG
      S  D  V  G  E  Y  R  A  V  T  E  L  G  R  P  D>
----->-----<-----

    340      350      360      370      380
    *      *      *      *      *
GCC GAC TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC
CGG CTC ATG ACC TTG TCG GTC GGC CTC TAG GAC CTC GCT TCG GCC CGG
      A  E  Y  W  N  S  Q  P  E  I  L  E  R  T  R  A>
----->-----<-----

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FIGURE 28 (SHEET 2 OF 4)

```

390      400      410      420      430
  *      *      *      *      *
GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC
CTC CAC CTG TGC CGC ACG TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG
E V D T A C R H N Y E G P E T S>
-----

440      450      460      470      480
  *      *      *      *      *
ACC TCC CTG CCG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC
TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CCG TAG AGG GAC AGG
T S L R R L E Q P N V A I S L S>
--- I-Ad β-1 domain --><----- I-Ad β-2 domain -----

490      500      510      520      530
  *      *      *      *      *
AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA
TCC TGT CTC CGG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT
R T E A L N H H N T L V C S V T>
-----

540      550      560      570
  *      *      *      *
GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG
CTA AAG ATG GGT CGG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC
D F Y P A K I K V R W F R N G Q>
-----

580      590      600      610      620
  *      *      *      *      *
GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC
CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG
E E T V G V S S T Q L I R N G D>
-----

630      640      650      660      670
  *      *      *      *      *
TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA
ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TCG GGA GTA GTC CCT
W T F Q V L V M L E M T P H Q G>
-----

680      690      700      710      720
  *      *      *      *      *
GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG ACC CCC ATC
CTC CAG ATG TGG ACG GTA CAC CTC GTA GGG TCG GAC TTC TCG GCG TAG
E V Y T C H V E H P S L K S P I>
----- I-Ad β-2 domain -----

730      740      750      760      770
  *      *      *      *      *
ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC
TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG
T V E W T S G G G G S G G G G S>
-----><----- 24 amino acid linker -----

```

FIGURE 28 (SHEET 2 OF 4)

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FIGURE 28 (SHEET 3 OF 4)

```

      780      790      800      810
      *      *      *      *
GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCG AGT GAA GAC GAC ATT
CCA CCG CCG CCA AGA CCG CCA CCG CCA ACG AGC TCA CTT CTG CTG TAA
G  G  G  G  S  G  G  G  G  S  S  S  E  D  D  I>
-----><-----

820      830      840      850      860
      *      *      *      *      *
GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT
CTC CCG CTG GTG CAT CCG AAG ATA CCA TGT TGA CAA ATA GTC AGA GGA
E  A  D  H  V  G  F  Y  G  T  T  V  Y  Q  S  P>
----- I-Ad α-1 domain -----

870      880      890      900      910
      *      *      *      *      *
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC
CCT CTG TAA CCG GTC ATG TGT GTA CTT AAA CTA CCA CTA CTC AAC AAG
G  D  I  G  Q  Y  T  H  E  F  D  G  D  E  L  F>
-----

920      930      940      950      960
      *      *      *      *      *
TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT
ATA CAC CTG AAC CTA TTC TTC TTT TGA CAG ACC TCC GAA GGA CTC AAA
Y  V  D  L  D  K  K  K  T  V  W  R  L  P  E  F>
-----

970      980      990      1000      1010
      *      *      *      *      *
GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT
CCG GTT AAC TAT GAG AAA CTC GGG GTT CCA CCT GAC GTT TTG TAT CGA
G  Q  L  I  L  F  E  P  Q  G  G  L  Q  N  I  A>
-----

1020      1030      1040      1050
      *      *      *      *
GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC
CGT CTT TTT GTG TTG AAC CCT TAG AAC TGA TTC TCC AGT TTA AAG TGG
A  E  K  H  N  L  G  I  L  T  K  R  S  N  F  T>
----- I-Ad α-1 domain -----

1060      1070      1080      1090      1100
      *      *      *      *      *
CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT
GGT CGA TGG TTA CTC CGA GGA GTT CGC TGA CAC AAG GGG TTC AGG GGA
P  A  T  N  E  A  P  Q  A  T  V  F  P  K  S  P>
-----><----- I-Ad α-2 domain -----

1110      1120      1130      1140      1150
      *      *      *      *      *
GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC
CAC GAC GAC CCA GTC GGG TTG TGG GAA TAG ACG AAA CAC CTG TTG TAG
V  L  L  G  Q  P  N  T  L  I  C  F  V  D  N  I>
-----

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FIGURE 28 (SHEET 4 OF 4)

1160 1170 1180 1190 1200
 TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AAG AAG TCA GTL
 AAG GGT GGA CAC TAG TTG TAG TGT ACC GAG TCT TTA TCG TTC AGT CAG
 F P P V I N I T W L R N S K S V>

1210 1220 1230 1240 1250
 ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC
 TGT CTG CCG CAA ATA CTC TGG TCG AAG GAG CAG TTG GCA CTG GTA AGG
 T D G V Y E T S F L V N R D H S>

1260 1270 1280 1290
 TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT
 AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA
 F H K L S Y L T F I P S D D D I>

1300 1310 1320 1330 1340
 TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA
 ATA CTG ACC TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTT
 Y D C K V E H W G L E E P V L K>

----- I-Ad α -2 domain -----

1350 1360 1370 1380 1390
 CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG CTG ACA GAA ACT
 GTG ACC CTT GGA CTC TAA GGT CCG GCG TAC AGT CTC GAC TGT CTT TGA
 H W E P E I P A P M S E L T E T>

----- I-Ad α -TM domain -----

1400 1410 1420 1430 1440
 GTG GTG TGT GCC CTG GGG TTG TCT GTG GGC CTT GTG GGC ATC GTG GTG
 CAC CAC ACA CCG GAC CCC AAC AGA CAC CCG GAA CAC CCG TAG CAC CAC
 V V C A L G L S V G L V G I V V>

1450 1460 1470 1480 1490
 GGC ACC ATC TTC ATC ATT CAA GGC CTG CGA TCA GGT GGC ACC TCC AGA
 CCG TGG TAG AAG TAG TAA GTT CCG GAC GCT AGT CCA CCG TGG AGG TCT
 G T I F I I Q G L R S G G T S R>

1500
 CAC CCA GGC CCT TTA TGA
 GTG GGT CCC GGA AAT ACT
 H P G P L ">
 - I-Ad α -TM domain ->

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FIGURE 29 (SHEET 1 OF 4)

```

      10      20      30      40      50
      *      *      *      *      *
CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC TCA GCT GCT GTG GTG
GGTGG TAC CGA GAC GTC TAG GGG TCG GAG GAG GAG AGT CGA CGA CAC CAC
      M  A  L  Q  I  P  S  L  L  L  S  A  A  V  V>
<----- I-Ad β chain leader ----->

      60      70      80      90
      *      *      *      *
GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
CAC GAC TAC CAC GAC TCG TCG GGT TCC TGG AAT TCA TAG AGA GTC CGA
      V  L  M  V  L  S  S  F  R  T  L  S  I  S  Q  A>
----->-----<-----

100      110      120      130      140
      *      *      *      *      *
GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
CAA GTG CGA CGA GTG CSA CTT TAG TTG CTT CGA CCA GCA CGA TCG CCT
      V  H  A  A  H  A  E  I  N  E  A  G  R  A  S  G>
----- OVA 323-339 ----->-----<-----

150      160      170      180      190
      *      *      *      *      *
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
CCC CCG CCT TCG CCG CCT CCC CCT TTG AGG CTT TCC GTA AAG CAC CAG
      G  G  G  S  G  G  G  G  N  S  E  R  H  F  V  V>
-- 10 amino acid linker --->----- I-Ad β-1 domain -----<-----

200      210      220      230      240
      *      *      *      *      *
CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG
GTC AAG TTC CCG CTC ACG ATG ATG TGG TTG CCC TGC GTC GCG TAT GCC
      Q  F  K  G  E  C  Y  Y  T  N  G  T  Q  R  I  R>
----->-----<-----

250      260      270      280      290
      *      *      *      *      *
CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC
GAG CAC TGG TCT ATG TAG ATG TTG GCC CTC CTC ATG CAC GCG ATG CTG
      L  V  T  R  Y  I  Y  N  R  E  E  Y  V  R  Y  D>
----->-----<-----

300      310      320      330
      *      *      *      *
AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC
TCG CTG CAC CCG CTC ATG GCG CGC CAC TGG CTC GAC CCC GCC GGT CTG
      S  D  V  G  E  Y  R  A  V  T  E  L  G  R  P  D>
----->-----<-----

340      350      360      370      380
      *      *      *      *      *
GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC
CGG CTC ATG ACC TTG TCG GTC GCG CTC TAG GAC CTC GCT TGC GCC CGG
      A  E  Y  W  N  S  Q  P  E  I  L  E  R  T  R  A>
----->-----<-----

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FIGURE 29 (SHEET 1 OF 4)

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FIGURE 29 (SHEET 2 OF 4)

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390      400      410      420      430
GAG GTG GAC ACC GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC
CTC CAC CTG TGC CGC ACC TCT GTG TTG ATG CTC CCC GGC CTC TGG TCG
E V D T A C R H N Y E G P E T S>
-----

440      450      460      470      480
ACC TCC CTG CCG CCG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC
TGG AGG GAC GCC GCC GAA CTT GTC GGG TTA CAG CCG TAG AGG GAC AGG
T S L R R L E Q P N V A I S L S>
--- I-Ad β-1 domain -->----- I-Ad β-2 domain -----

490      500      510      520      530
AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA
TCC TGT CTC CCG GAG TTG GTG GTG TTG TGA GAC CAG ACA AGC CAC TGT
R T E A L N H H N T L V C S V T>
-----

540      550      560      570
GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG
CTA AAG ATG GGT CCG TTC TAG TTT CAC GCG ACC AAG TCC TTA CCG GTC
D F Y P A K I K V R W F R N G Q>
-----

580      590      600      610      620
GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGC GAC
CTC CTC TGT CAC CCC CAG AGT AGG TGT GTC GAA TAA TCC TTA CCC CTG
E E T V G V S S T Q L I R N G D>
-----

630      640      650      660      670
TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA
ACC TGG AAG GTC CAG GAC CAG TAC GAC CTC TAC TGG GGA GTA GTC CCT
W T F Q V L V M L E M T P H Q G>
-----

680      690      700      710      720
GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC
CTC CAG ATG TGG ACG GTA CAC CTC GTA GCG TCG GAC TTC TCG GCG TAG
E V Y T C H V E H P S L K S P I>
----- I-Ad β-2 domain -----

730      740      750      760      770
ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC
TGA CAC CTC ACC TGA TCA CCA CCG CCA CCG TCG CCG CCA CCA CCA AGG
T V E W T S G G G G S G G G G S>
-----><----- 24 amino acid linker -----

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[illegible]

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FIGURE 29 (SHEET 4 OF 4)

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      1160      1170      1180      1190      1200
      *        *        *        *        *
TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC
AAG GGT CGA CAC TAG TTG TAG TGT ACC GAG TCT TTA TCG TTC AGT CAG
P  P  P  V  I  N  I  T  W  L  R  N  S  K  S  V>
-----

      1210      1220      1230      1240      1250
      *        *        *        *        *
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC
TGT CTG CCG CAA ATA CTC TCG TCG AAG GAG CAG TTG GCA CTG GTA AGG
T  D  G  V  Y  E  T  S  F  L  V  N  R  D  H  S>
-----

      1260      1270      1280      1290
      *        *        *        *
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT
AAG GTG TTC GAC AGA ATA GAG TGG AAG TAG GGA AGA CTA CTA CTG TAA
F  H  K  L  S  Y  L  T  F  I  P  S  D  D  D  I>
-----

1300      1310      1320      1330      1340
      *        *        *        *        *
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA
ATA CTG ACG TTC CAC CTC GTG ACC CCG GAC CTC CTC GGC CAA GAC TTT
Y  D  C  K  V  E  H  W  G  L  E  E  P  V  L  K>
----- I-Ad α-2 domain -----

      1350      1360      1370      1380
      *        *        *        *
CAC TGG GAG GAA GAA GAG TAC ATG CCG ATG GAA TGA
GTG ACC CTC CTT CTT CTC ATG TAC GGC TAC CTT ACT
H  W  E  E  E  E  Y  M  P  M  E  *>
-----> EE tag ----->

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